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A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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                                          EMBL; AK057778; BAB7155
EMBL; BC004417; AAH0441
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Herrmann J., Wu J.C., Fesik S.W.;
"Structural basis for binding of Smac/DIABLO to
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[7]
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MEDLINE-20426096; PubMed=10972280;
Chai J., Du C., Wu J.W., Kyin S., Wang
"Structural and biochemical basis of a
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                                                                                                                                                                                                                                                                    tities requires a license agreement (S send an email to license@isb-sib.ch).
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L; AK024708; BAB14994.1;
L; AF29870; AAG22077.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The mature
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SUBCELLULAR LOCATION: MITOCHONDRIAL BUT RELEASED WHEN CELLS UNDERGO APOPTOSIS.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                   BIRC4/XIAP.
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DOMAIN: The mature N-terminus mediates interaction
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TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED WITH HIGHEST EXPRESSION IN TESTIS. EXPRESSION IS ALSO HIGH IN HEART, LIVER, KIDNEY, SPLEEN, PROSTATE AND OVARY. LOW IN BRAIN, LUNG, THYMUS AND
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                               peptide;
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                                       C:mitochondrion; TAS.

P:caspase activation via cytochrome
P:induction of apoptosis via death d
P:induction of apoptosis; TAS.
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/CASPASE-9 PATHWAY. ACTS BY OPPOSING
OF INHIBITOR OF APOPTOSIS PROTEINS (
Interacts with BIRC2, BIRC3, BIRC4/)
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                             Apoptosis;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouakenbush J.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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                                                                                                                                                           Wilming L., 'Kohtsuki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/C: TIDSUB-NAMEDINE-2038353; PubMed=10929712; MEDLINE-20383537; PubMed=10929712; Verhagen A.M., Ekert P.G., Pakusch M., Silke J. Reid G.E., Moritz R.L., Simpson R.J., Vaux D.L. "Identification of DIABLO, a mammalian protein "Identification of DIABLO, a mammalian protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMAC_MOUSE STANDARD; PRT; 237 AA.

(99JIQ3; Q9CZD1; Q9DCD3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Smac protein, mitochondrial precursor (Second mitochondria-derived activator of caspase) (Direct IAP binding protein with low pI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
                                                                                                      "Functional annotation o Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by binding to and antagonizing IAP Cell 102:43-53(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
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  INHIBITORY ACTIVITY OF INHIBITOR SUBUNIT: Homodimer. Interacts wi
                                                  FUNCTION: PROMOTES APOPTOSIS BY ACTIVATING CASPASES IN THE CYTOCHROME C/APAF-1/CASPASE-9 PATHWAY. ACTS BY OPPOSING TH
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  Interacts with BIRC2,
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/FTId=VSP_004397.
K -> E (IN REF. 4).
K -> R (IN REF. 2).
MISSING (IN REF. 4).
E -> K (IN REF. 4).
W; 70C2AE0DC654D031 C
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MAALKSWLSRSVTSFERYRQCLCVPVVANFKKRCFSELIRP

WKKTVTIGFGVTLCAVPIA -> MKSDFYF (in
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Pred. No. 3e-14;
Mismatches
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                      OF APOPTOSIS PROTEINS
                                                                                                                               mouse
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; Murinae; Mus
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RESULT 3
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AC 003718
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-SEP
Hypoth
GN YML023
OS Saccha
OC EUKary
OC Saccha
OX RACCHA
OX MCB1_1
RP SEQUEN
RX PUBMec
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Best Local
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01-NOV-1997
15-SEP-2003
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., 'Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Succharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
saccharomycetales; Saccharomycetaceae; Saccharomyces.
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TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
15-SEP-2003 (Rel. 42,
Hypothetical 64.0 kDa
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                              EMBL; Z46659;
PIR; S49754; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowman S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q03718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                         Nature 387:90-93(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: The mature N-terminus mediates interaction
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SUBCELLULAR LOCATION: MITOCHONDRIAL BUT RELEASED INTO THE CYTOSOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIRC4/XIAP (By similarity).
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54
64
237
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                                 ; CAA86632.1;
S49754.
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237 5
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26829 MW;
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Last annotation update)
protein in RPS17A-APT1
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IAP-BINDING MOTIF
H -> Q (IN REF. 2)
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RESULT 4
YNE2_CAEEL
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                                                                                                                                                                                                                                                                                                                                                      Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J. Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                          PIR; S41037; S24458.
WormPep; R08D7.2; CE00290.
Pfam; PF04181; DUF408; 1.
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical R08D7.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30641;
01-APR-1993
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TRANSMEM 61 81 POTENTIAL.
                                                                                                     SEQUENCE
                                                                                                                                                                   EMBL; Z12017; CAA78048.1;
                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                  elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNE2_CAEEL
                                                                                                                Hypothetical protein
                                                                                                                                                                                                                                                                                                                                             Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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PILRANDPYNTSRETLSRRALKLL 108
                                                                                                                                                                                                                                                                                                                               contiguous nucleotide sequence from chromosome
                                                                                                    455 AA;
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                                                                                                     52438 MW;
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Pred. No.
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                                                                           Score 51;
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                                                                                                     1FDFADAA58980F3E CRC64;
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RESULT 5
ELK1_MOUSE
ID ELK1_MOUSE

STANDARD;

PRT;

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Best Local
                                                     Matches
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PROSITE;
PROSITE;
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                                                                                                          SEQUENCE
                                                                                                                                     Phosphorylation.
DNA_BIND 5
                                                                                                                                                           Transcription regulation;
                                                                                                                                                                                                                PRINTS; PRO0454; ETSDOMAIN. SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                               TRANSFAC; T05013; -. MGD; MGI:101833; Elk1
                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                      EMBL; X87257; CAA60715.1; -. EMBL; Z36939; CAA85391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glovane A., Phitzas A., Maira S.-M., Sobieszczuk P., Wasylyk "Net, a new ets transcription factor that is activated by Ras Genes Dev. 8:1502-1513(1994).

-i- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grevin D., Ung S., Denhez F., Dehem Stehelin D., Martin P.; "Structure and organization of the Gene 174:185-188(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ETS-domain protein ELK-1.
                                                                                                                                                                                                                                           Pfam; PF00178; Ets;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=97017146; PubMed=8863747;
Grevin D., Ung S., Denhez F., Dehem M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P41969;
01-NOV-1995
                                                                                                                                                                                                                                                     InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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MEDLINE-95047310; PubMed=7958835;
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                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN
LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                           JC4965; JC4965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
270
                          S
                                                     10;
                                                                Similarity
                                                                                                                                                                         PS00345;
PS00346;
PS50061;
              AQKSEPHSLSSEALMRRAVSLVTDST
AVKAEPEVSASEGLLARLPAILTENT
                                                                                                         429 AA;
                                                                                                                         133
                                                   Conservative
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ETS_DOMAIN_2; 1.
ETS_DOMAIN_3; 1.
                                                                                                                       86
133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORM A TERNARY COMPLEX WITH
                                                                                                          45243 MW;
                                                                35.5%;
                                                               3.5%;
                                                                                                                                                            Activator; Nuclear
                                                  8;
                                               Score 50; DB Pred. No. 5.3; 8; Mismatches
                                                                                                                    ETS-DOMAIN.
P -> T (IN REF
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                                                                                                       B61B5B977731D54F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse
                       30
                                                            DB
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                                                                                                                                                          protein;
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                                                                             Length 429;
                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE
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ed by Ras.";
                                                                                                                                                          DNA-binding;
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RESULT 6 YI38_MYCTU

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RESULT 7
LINC_PSEPA
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Best Local S
Matches 11
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy, A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
N Rature 393:537-544(1998).
 LINC_PSEPA
P50197;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                InterPro; iraccing from Pfam; PF01850; PIN; 1.
SMART; SM00670; PINC; 1.
SMART; Sm00670; PINC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                        TubercuList; Rv1838c; ... InterPro; IPR002716; PIN. InterPro; IPR006596; PINc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg (
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula /
                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 1:
                                                                                                                                                                                                                                                                                                                                                                                           TIGR; MT1886;
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z83859; CAB06116.1; -. EMBL; AE007047; AAK46157.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actino
Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           F70663; F70663.
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                                                                                                                                                                                                                        Similarity
                                                                                                                                     SHPHKLDAQRLLESALSGGERLVTDA 41
                                                                                                                                                                   SEPHSLSSEALMRRAVS----LVTDS 29
                                                                                                                                                                                                                                                                         11 protein;
131 AA; 1
                                                                                                                                                                                                        Conservative
                                                  STANDARD;
                                                                                                                                                                                                                                                                         14726 MW;
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Created)
sequence update)
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Pred. No. 3
                                                  PRT;
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C164346E951BFE7E CRC64;
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28-FEB-2003
15-SEP-2003
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
"Cloning and sequencing of a 2.5-dichloro-2.5-cyclohexadiene-1.4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";
J. Bacteriol. 176:3117-3125(1994).
-!- FUNCTION: DEGRADATION OF 2.5-DICHLORO-2.5-CYCLOHEXADIENE-1.4-DIOL
(2.5-DDOL) INTO 2.5-DICHLOROHYDROQUINONE (2.5-DCHQ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00080; SDRFAMILY.

PROSITE; PS00061; ADH_SHORT; 1.

Aromatic hydrocarbons catabolism; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D14595; BAA03444.1; -. HSSP; P19992; 1HDC. InterPro; IPR002198; ADH_short. Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long amodified and this statement is not removed.
                    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                      STRAIN-C57BL/6J; TISSUE-Mammary gland; meDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                              C220RF4.
                                                                                                                                                                                                                                                                                                                                                  TBC1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8R5A6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CV04_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94252977; PubMed-7515041; Nagata Y., Ohtomo R., Miyauchi K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonadaceae;
NCBI_TaxID=13689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (2,5-DDOL dehydrogenase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (Se an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIGRESEPHEQAQAAVWLLSDAASEVTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIAOKSEPHSLSSEA--LMRRAVSLVTDS
                                                                                                                                                                                                                                                                                                                                             3 (Rel. 41, Created)
3 (Rel. 41, Last sequence of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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25644 MW;
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                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%;
  K., Farmer A.A.,
                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
C22orf4 homolog (Fragment).
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Pred. No.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFC1CAEB47DF789D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb~sib.ch/announce/
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  Rubin G.M.,
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                                      G.D.,
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             003631;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Putative 107.6 kDa transcriptional regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC023106; AAH23106.1; ALT_INIT.
InterPro; IPR00195; RabGAP_TBC.
Pfam; PF00566; TBC; 1.
SMART; SM00164; TBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     STRAIN=S288c /
PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton M., Soares M.B.,
                                                                 -!- SUBCELLULAR
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        YML076C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMH6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                              Nature 387:90-93(1997)
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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SIMILARITY: Contains 1 Rab-GAP TBC domain.
                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                            / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                    Contains
                                                             LOCATION: Nuclear (Probable). Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TBC_RABGAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
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39.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAB-GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB-GAP TBC.
B16BD293761D4A53 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
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                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Carninci P., Prange C.,
Abramson R.D., Mullahy S.J.,
Malek J.A., Gunaratne P.H.,
a A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPR3-HMG1
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P58397;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.; "Identification, characterization, and intracellular processing ADAM-TS12, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats."; J. Biol. Chem. 276:17932-17940(2001).

-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracel
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MEDLINE=21264577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAMTS-12 precursor (EC 3.4.24..) (A disintegrin and metwith thrombospondin motifs 12) (ADAM-TS 12) (ADAM-TS12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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PROSITE; PS50048; ZN2_CY6_FUNGAL_2; FALSE_NEG.

Hypothetical protein; Transcription regulation; DNA-binding;

Nuclear protein; Metal-binding.

DNA_BIND 76 109 ZN(2)-CYS(6), FUNGAL-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S48821; S48821.
SGD; S0004541; YML076C.
InterPro; IPR001138; Fungi_TrN.
SMART; SM00066; GAL4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                             SIMILARITY: Belongs to peptidase family SIMILARITY: Contains 1 disintegrin. like SIMILARITY: Contains 1 PLAC domain.
SIMILARITY: Contains 8 TSP type-1 domain
                                                                                                                                                                                                                                                                                                              PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE. PTM: IS SUBJECTED TO AN INVERGEBLULUE MATURATION PROCESS TO A FRACMENT CONTAINING THE N-TERMINAL REGION INCLUDING METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: THE SPACER DOMAIN AND FOR A TIGHT INTERACTION WITH T SIMILARITY).
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TISSUE SPECIFICITY: Exp
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ROT entry is copyright. It is prod
Swiss Institute of Bioinformatics
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v; 020A56745DF52CCC
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Matches 12
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PROSITE; PS00142; Hydrolase; Metallor
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CARBOHYD
CARBOHYD
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Pfam; PF01562; Pep_misp_r.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 6.
Pfam; PF00090; Tsp_1; 8.
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213 SVNISQKQELWREKWERHNLPSRSLSRRSIS
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PS00427;
PS50214;
                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix.
                AVPIAQKS-----
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IPR006025; Zn_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001762; Disintegrin.
IPR002870; Pep_M12B_propep.
IPR001590; Reprolysin.
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1312
1367
1422
1471
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951
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393
                               Conservative
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Pep_M12B_propep; 1.
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A; 177545
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125
215
2485
685
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1104
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1300
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1371
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942
996
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1365
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1593
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N-LINKED (GLCNAC...
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MW; 07F9F48E63BD83A3
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PLAC.
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CYS-RICH.
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TSP TYF
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TYPE-1
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TYPE-1
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NKED (GLCNAC.
                             e 45.5; I
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ismatches
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RESULT 11
VAF2_DROME
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RA Adams N.D., Celniker S.E., Hil F.M., Hoskins R.A., Galle R.F.,
RA Adams N.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Ffeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Carcell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hortis N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lai Z., Lai Z., Liang Y., Lin X.,
Lai Z., Liang Y., Lin X.,
Lai Z., Liang Y., Lin X.,
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RA Mount S.M., Moy M., Murphy L., Mu
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable vacuolar ATP synthase subunit F 2 (EC 3.6.3.14) (V-ATPase subunit 2) (Vacuolar proton pump F subunit 2) (V-ATPase 14 kDa subunit 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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16-OCT-2001
                       This SWISS-PROT entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAF2_DROME
                                                                                   peripheral catalytic V1 an integral membrane V0 c'' and d) 'Po ~'-''
                                                                                                                                                                              FUNCTION: SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF VACUOLAR ATPASE ESSENTIAL FOR ASSEMBLY OR CAPALYTIC FUNCTION. V-ATPASE IS RESPONSIBLE FOR ACCIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENT: IN EUKARYOTIC CELLS (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                              SIMILARITY:
                                                                                                                                              H(+)(Out).
SUBUNIT: V-ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 40, Created)
      Swiss
                                                                                 (By similarity)
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                                                            Belongs to the V-ATPase F subunit family
    Institute
  is copyright. It is produstitute of Bioinformatics
                                                                                                    proton
                                                                                                                           complex (components
                                                                                                                                              heteromultimeric
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produced through a collaboration atics and the EMBL outstation -
                                                                                                                                            enzyme
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                                                                                                                           H) attached
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RESULT 12

NRED_ECOLI

ID NRED_ECOLI

AC p32709;

DT 01-CCT-1993

DT 01-CCT-1993

DT 01-CCT-1993

DT 16-CCT-2001

DE NRED OR BACTETIA;

PR SEQUENCE FRC

RX MEDLINE=943;

RA HUSSAIN H.A.

RT "A Seven-ger

RT reduction to

RT "FRAIN=K12,

RR SEQUENCE FRC

RY MEDLINE=940;

RR (2)

RR SEQUENCE FRC

RY MEDLINE=940;

RR ABLATCHOR FR

RD SEQUENCE FRC

RT "Analysis on

RT "Analysis on

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RT "SUBCELLI

CC -i- FUNCTION

CC -i- SUBCELLI

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01-OCT-1993
01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0037402; CG1076.
InterPro; IPR005772; ATPSynt_Feuk.
InterPro; IPR002641; ATPSynt_Fsub.
Pfam; PF01990; ATP-synt_F; 1.
ProDom; PD003811; ATPSynt_F; 1.
TIGRPAMS; TIGR01101; V_ATP_synt_F; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 124 AA; 14132 MW; 0C5093AFDF0006BAB C
                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 21:5408-5417(1993).

-i- FUNCTION: PROBABLY INVOLVED IN THE TRANSFER OF EI
OUINONE POOL TO THE TYPE-C CYTOCHROMES.

-i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A seven-gene operon essential for formate-dependent nitrite reduction to ammonia by enteric bacteria.";
Mol. Microbiol. 12:153-163(1994).
                                                                                                                                                    entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94335626; PubMed=8057835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NrfD protein.
NRFD OR B4073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Some or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daniels D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner F.R., Burland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94089392; PubMed=8265357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation-European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content in institutions as long as its content in its
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
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                                                X72298; CAA51044.1;
U00006; AAC43167.1;
AE000480; AAC77043.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
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                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
TBC1 domain family protein C22orf4 homolog (Q
                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                  PROSITE; PS50086; TBC_RABGAP; 1.
                                                                                                                                                                                                                                              Pfam; PF00566; TBC; 1
SMART; SM00164; TBC;
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InterPro; IPR000195; R
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TRANSMEM
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                      EMBL; AB060857; BAB46876.1; ALT_INIT
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497 AA;
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                                                                         Score 45; DB
Pred. No. 37;
3; Mismatches
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                                                                                                                                                     RAB-GAP TBC.
; 47EF1098A998937A CRC64;
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-> A (IN REF. 2).
BC5B3EF031D5CE29 CRC64;
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                                                                                                               DB 1; Length 497;
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TUD_DROME
                                                                                         Matches
                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0003891; tud.
GO; GO:0019090; P:mitochondrial rRNA, mitochondrial export;
GO; GO:0007315; P:pole plasm assembly; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00333; TUDOR; 10.
PROSITE; PS50304; TUDOR; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00567; TUDOR; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X62420; CAA44286.1; -. PIR; A41519; A41519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Golumbeski G.S., Bardsley A., Tax F., Boswell R.E., "Tudor, a posterior-group gene of Drosophila melanogaster, novel protein and an mRNA localized during mid-oogenesis.", Genes Dev. 5:2060-2070(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUD
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01-MAY-1992 (Rel. 22,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001097; Maternal_tudor
InterPro; IPR002999; Tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q16637; 1G5V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 9 Tudor domains.
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8; Conser
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1355
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2023
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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                                                                                    Score 45; DB Pred. No. 2.5e 7; Mismatches
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RESULT 15
DPOZ_MOUSE
ID DPOZ_MOUSE

STANDARD;

PRT;

3122 AA.

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THEFT THE TOTAL DRAW THE PROPERTY OF THE PROPE
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R InterPro; IPR006134; DNA_pol_B_dom.
R InterPro; IPR006133; DNA_pol_B_exo.
R InterPro; IPR006133; DNA_pol_B_exo.
R InterPro; IPR004578; Pol2.
R Pfam; PF00136; DNA_pol_B; 1.
R Pfam; PF03104; DNA_pol_B_exo; 1.
R Pfam; PF03104; DNA_pol_B_exo; 1.
R PRINTS; PR00106; DNAPOLB.
N PRINTS; SM00486; POLBC; 1.
NR PRINTS; SM00486; POLBC; 1.
NR TIGREAMS; TIGRO0592; Pol2; 1.
NR TIGREAMS; TIGRO0592; Pol2; 1.
NR TIGREAMS; TIGRO0592; DNA_POLYMERASE_B; 1.
NR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
NR TIGREAMS; DNA_directed DNA_polymerase; DNA_replication;
NW Transferase; DNA_repair; Nuclear proretin; Zinc-finger.
NATURE OF TRANSPORT OF TRANSPORT
                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differential screening.";
Biochem. Biophys. Res. Commun. 219:795-799(1996).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              061493; Q9JMD6; Q9QWX6;
30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (Seizure related
    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                 ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugaya E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kajiwara K., Nagawawa H., Shimizu-Nishikawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brain neurons."
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STRAIN=129/Ola; TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular analyses of Sez4 encoding murine homologue of yeast REV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kajiwara
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                                                                                       CONFLICT
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-> T (IN REF. 2).
-> Q (IN REF. 2).
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CONFLICT
SEQUENCE
1226 AIPADEKMKPHSEAELTPNHQSVSELTSSS 1255
           1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
                                10;
                                       Similarity
                                                                1848
2368
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                                Conservative
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2368
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Pred. No. 3
                                 Mismatches
                                                               > T (IN REF. 2).
> G (IN REF. 3).
A39846CAF7365BA8 CRC64;
                                               DB 1;
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Search completed: October Job time: 24 secs

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2003, 09:37:22

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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primard is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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AAU78435
AAU78436
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                         Inhibitor of apopt
Human partial sequ
Human pancreatic c
Human caspase acti
Inhibitor of apopt
                                                                                                                                                                                                                                                                                                                                                          Description
   Human DIABLO/Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              being printed,
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4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	5	14	3		11	10
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31.9						•				31.9		٠	•	•	•									33.3		35.5	39.7	44.7		49.6		83.7		97.9	100.0
2161	2038	1018	809	809	809	809	809	644	355	173	124	44	182	594	499	384	352	336	312	312	284	272	2045	944	710	396	73	13	13	15	20	186	84	237	239
2.2	23	22	23	23	23	23	23	22	23	22	22	22	22	22	21	21	23	22	24	22	23	22	22	23	23	22	24	24	24	24	23	22	24	24	24
AAM/8959	AAE25098	ABB62522	AAE15986	AAE15985	AAE15984	AAE15983	AAE15982	ABG05466	ABP66105	AAU48666	ABB57798	ABB12208	ABU53172	ABB61195	AAG41345	AAG54380	ABP29265	AAU27891	ABP55411	AAU27719	ABG79600	AAG66438	ABB61941	ABP35704	ABP69647	AAU51015	ABG72304	ABG72316	ABG72314	ABP71314	ABB76208	AAB92922	ABG72303	ω	ABB82743
Human protein SEQ	Human kinase and p	Drosophila melanog	Human CNG3B protei		CNG3B	סי	-	Novel human diagno	Bifidobacterium lo	Propionibacterium	Drosophila melanog	Human secreted pro	Human testes-deriv	=		Arabidopsis thalia	tococcus	contig p	Human MDDT-20 prot	Human full-length	Vernonia ribonucle	Human ATPase 30.	hila	Fungal ZBC protein	Human polypeptide		Q.	_	pro-a	Smac		n protei	a	pro-a	Human Smac polypep

ALIGNMENTS

RESULT 1 AAU78435

AAU78435 standard; Peptide; 30

AAU78435;

18-JUN-2002 (first entry)

Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N30.

Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; mutant; tumour.

Homo sapiens

Synthetic.

28-FEB-2002

WO200216418-A2

24-AUG-2001; 2001WO-US26492

24-AUG-2000; 2000US-227735P.

(UYJE-) UNIV JEFFERSON THOMAS

Alnemri

WPI; 2002-304115/34

Novel Smac peptides and polynucleotides encoding the peptides, useful

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RESULT 2
AAU78439
ID AAU7
XX
AC AAU7
XX
ID 18-J
XX
Inhi
XX
IN Huma
KW Huma
KW Heop
XX
IN Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Creplacing the mitochondrial targeting sequence (residues 1-55 of (I)), and an inhibitor of BID (Bcl2 interacting cd domain) with a compound to be tested for apoptotic inhibiting activity; (C) (b) incubating the cell populations with a direct stimulus of the cell populations, where inhibition of the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is cell populations, where inhibitor of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase. Where the cell polynucleotide are useful for stimulating apoptosis in a neoplastic or caspase. Perferably, the cell overexpresses at least a portion of IAP. (I) suseful for identifying an inhibitor of caspase. Where the cell is useful for identifying an inhibitor or enhancer of a caspase. (I) and (II) is useful for identifying an inhibitor or enhancer of a caspase. (I) and (II) transferred or captase and an expressing (I) with a candidate inhibitor or call viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in the processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an
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24-AUG-2001; 2001WO-US26492
                                                                               28-FEB-2002
                                                                                                                                                 WO200216418-A2
                                                                                                                                                                                                                                                                                          neoplastic cell;
                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor of apoptosis (IAP) protein Smac, peptide Smac-N35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU78439 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 7; 78pp; English
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                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                   n; inhibitor of apoptosis; IAP; Smac;
interacting domain; caspase; BIR domain; caspase; BIR domain; caspase; BIR domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Pred. No. 2.2e-16;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                    mac; apoptosis; BID; BIR1; BIR2;
domain; BIR3; gene therapy;
                                                                                                                                                                                                                                                                                                             BIR3; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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RESULT 3 AAU78436

AAU78436 standard; Peptide;

DЬ

1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST

0,

18-JUN-2002 AAU78436;

(first entry)

Human; inhibitor of apoptosis; TAP; Smac; apoptosis; BID; BIR1; BIR2;

Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N39

```
Q
                                                                                                                                                                                                                               CC transfected with a vector expressing (I) with a candidate inhibitor or CC candidate enhancer; and detecting cell viability, where an increase in CC cell viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an enhancer. Optionally, the CC method involves detecting the presence of large and small caspase CC subunits after contacting cell transformed with the vector expressing CC (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for CC ciapnitying a compound that inhibits Smac binding to Smac-binding CC molecule (a portion of IAP e.g. a BIR domain such as BIRI, BIR2 or BIR3, CC or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the amino acid sequence of Smac peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to an isolated Smac peptide or polypeptide (I) CC and an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BCl2 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity; (C) incubating the cell populations with a direct stimulus of the cell (CC (b) incubating the cell populations with a direct stimulus of the cell cell pathway; and (c) measuring the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is CC indicative that the compound is an inhibitor of apoptosis. (I) and (II) CC are useful for inducing apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transformed or transforted with a vector expression (I) with a capitate inhibitor or enhancer.
                                                                          Matches
                                                                                               Query Match
Best Local (
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 47; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for stimulating apoptosis in neoplastic overexpresses inhibitor of caspase, and modulating compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000; 2000US-227735P
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                                                                                               Local Similarity
1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
                                                                          30;
                                                                                                                                                                       35
                                                                        Conservative
                                                                                                                                                                       ΑA;
                                                                                               100.0%;
                                                                     0;
                                                                Score 141; DB 23;
Pred. No. 2.7e-16;
                                                                                                                 Length
                                                                     0,
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CC (a) separately contexting several cell populations appects, comprising:
CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)),
CC and residues 56-60 of (J)) and an inhibitor of BID (BI2 interacting
CC domain) with a compound to be tested for apoptotic inhibiting activity;
CC (b) incubating the cell populations with a direct stimulus of the cell
CC death pathway; and (c) measuring the specific apoptotic activity of the
CC cill populations, where inhibition of the specific apoptotic activity is
CC indicative that the compound is an inhibitor of apoptosis. (I) and (II)
CC are useful for inducing apoptosis in a cell. The Smac polypeptide and
CC polynucleotide are useful for stimulating apoptosis in a neoplastic or
CC tumour cell which overexpresses an inhibitor of caspase-3, caspase-7 or
CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP.
CC (I) is useful for identifying an inhibitor or enhancer of a caspase-
CC mediated apoptosis which involves contacting a cell transformed or
CC call viability indicates the presence of an inhibitor or
CC call viability indicates the presence of an enhancer. Optionally, the
CC method involves detecting the presence of an enhancer optionally, the
CC caspase-3, caspase-7 or caspase-6 of an inhibitor and an increase in the processing indicates the
CC presence of an inhibitor and an increase in the processing indicates the
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC caspase-1 and caspase-1 or ca
                                                                                         Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis
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neoplastic cell;
                                                                                                                                                                                Sequence
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                                                                                                              Similarity
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AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
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                                                                                                                                                                                  39
                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain; caspase; BIR domain; BIR3; gene therapy;
mutant; tumour.
                                                                                                                                                                                                                                             IAP). (II) is useful in gene therapy techniques. '
represents the amino acid sequence of Smac mutant
                                                                                                              100.0%;
                                                                                           0
                                                                                         Score 141; DB 23; Pred. No. 3.1e-16; ); Mismatches 0;
                                                                                                                                   Length
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Sequence

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AAU78430
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AAU79430
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AAU79
                                                                                            The invention relates to an isolated Smac peptide or polypeptide (I) cand an isolated nucleic acid (II) encoding (I). Also described is a comethod of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDPYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BCl2 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity of the cell conclusing the cell populations with a direct stimulus of the cell cell populations, where inhibition of the specific apoptotic activity of the CC cell populations, where inhibition of the specific apoptotic activity is condicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and CC polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase. Where the CC inhibitor inhibits activation or activity of caspase 3, caspase-7 or CC caspase 9. Preferably, the cell overexpresses at least a portion of IAP. CC ill visuation of the presence of an enhancer of a caspase-C mediated apoptosis which involves contacting a cell transformed or call viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an inhibitor and a decrease in CC cll viability indicates the presence of an inhibitor and a decrease in CC caspase-3, caspase-7 or caspase-6 are detected. (I) is also useful for caspase-7 or caspase-7 or caspase-7 or caspase-7 or caspase-8 in the processing indicates the presence of an inhibitor and small subunits of caspase-8 are detected. (I) is also useful for identifying a compound that inhibits small amino acid sequence of Smac C caspase-8 are detected. (I) is also useful for identificat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; inhibitor
Bc12 interacting
neoplastic cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis modulating compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU78430 standard; Peptide; 40 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Fig 7; 78pp; English
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RESULT 5
ABG72302
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Best Local
       binding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO relate condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological
                                                                                                                                              The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino aci in length. Also included are the polypucleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (I with a fragment of the polypeptide, and detecting a reduction in acti of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenwith cell death activity or which reduces IAP activity.
                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                 Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; neurodegenerative disease; hepatic muscular tissue damage; heart attack; hepatic tissue damage; liver disease; immunogen.
                                                                                                                                                                                                                                                                                                         death or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                                           modulate
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                                                                                                                                                                                                                                                                                                                                                                                            Verhagen AM,
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                                                                                                                                                                                                                                                                                                                      pro-apoptotic polypeptide, useful ulate cell death and for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
  which modulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                             50pp; English.
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                                                                                                                                                                                                                                                                                                                                     useful
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Pred. No. 3.2e-16;
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                                                                                                                                                                                 in activity
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                                                                   related
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of
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RESULT 6
AAB54139
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Best Local
           in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used
                                                                                         neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be u
                                                                                                                 AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic,
                                                                                                                                                                                  Claim 11; Page 1027-1028; 1379pp; English
                                                                                                                                                                                                                               New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autoimmune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack, or hepatic tissue damage associated with a liver disease. DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence
                                                                                                                                                                                                                                                                               N-PSDB; AAC98904
                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; likage analysis; tissue identification; tissue typing; forensic;
                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200055320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pulmonary; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neural;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pancreatic cancer antigen protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 AA;
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                                                                                                                                                                                                                  in
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Pred. No. 2.
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Query Match
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Best Local
                                                                     The present sequence is the human Smac protein. Its coding sequence was isolated by purifying the protein and searching a HeLa cell cDNA library for sequences which bound to probes based upon it. Smac is a mitochondrial protein which is released into the cytosol during apoptosis, and acts as a caspase-3 activator. The protein and its coding sequence can be used to modulate the expression and function of caspases and their activators, and also can be used as drug targets and regulators to promote or inhibit apoptosis in the treatment of cancer and autoimmune and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                       Novel caspase regulatory polypeptides useful for screening binding agents specific for the polypeptides which are useful for diagnosis and also for treating apoptosis associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6110691-A
                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caspase activator; Smac; apoptosis; cancer; autoimmune egenerative disease; mitochondria.
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                                                                                                                                                                                                                         column 23-24; 16pp;
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141; DB 21;
No. 3.3e-15;
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                                                                                     The invention relates to an isolated Smac peptide or polypeptide (I) CC and an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: CC (a) separately contacting several cell populations expressing a CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (BC12 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell cell populations, where inhibition of the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is condicative that the compound is an inhibitor of apoptosis. (I) and (II) CC indicative that the compound is an inhibitor of caspase. Where the cumbination or activity of caspase-3, caspase-7 or CC tumour cell which overexpresses an inhibitor of caspase-7 or CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (C i) is useful for identifying an inhibitor or enhancer of a caspase-CC mediated apoptosis which involves contacting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or candidate enhancer; and detecting cell viability, where an increase in CC cell viability indicates the presence of an inhibitor and a decrease in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the presence of an inhibitor and adecrease in CC cell viability indicates the cell compound. A decrease in processing indicates the compound in the cell cell cell cof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis modulating compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-304115/34
N-PSDB; ABK15451.
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    with the candidate compound. A decrease in processing indicates the
presence of an inhibitor and an increase in the processing indicates the
presence of an enhancer. Preferably, the large and small subunits of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002
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domain; BIR3; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 9
ABP72164
ID ABP72164
ID ABP72164
ID ABP72164
ID ABP72164
ID ABP7
XX ABP7
XX Huma
XX Huma
XX Homc
XX ITO
ABP7 LICE
XX ITO
AX ITO
ABP7 LICE
XX ITO
ABP7 LICE
ABP7 LICE
XX ITO
ABP7 LICE
ABP7 LICE
ABP7 LICE
ABP7 LICE
ABP7 
                                                                                                                                           The present sequence is the protein sequence for human DIABLO/Smac, an inhibitor of inhibitor-of-apoptosis (IAP) proteins. The invention provides a nucleic acid, such as an antisense coliquoucleotide, which specifically hybridises to a nucleic acid encoding a protein that induces cell death, especially APAFI, RAIDD or Diablo/SMAC. A claimed method for inhibiting a cell's death cell with the nucleic acid under conditions permitting the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a meromatical or electrical means. The method is used to a treat a neurodegenerative disorder, especially a brain disorder or central nervous system disorder, or a heart disorder, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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          Query Match
Best Local S
Matches 30
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Best Local S
Matches 30
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 23A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding molecule (a portion of IAP e.g. a BIR domain such as BIRI, BIR2 or BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the amino acid sequence of Smac protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; DIABLO/Smac; cell death; u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Troy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2002; 2002WO-US21002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DIABLO/Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP72164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP72164 standard;
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DB; ABZ58109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVPIAQKSEPHSLSSEALMRRAVSLYTDST
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                                                                                                                239
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding an inhibitor-of-apoptosis protein, useful neurodegenerative disorder or cardiomyopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
100.0%; SC
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell death; apoptosis;
lsease; heart disease; cardiomyopathy; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.
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  Score 141; DB 24;
Pred. No. 3.3e-15;
Mismatches 0;
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Pred. No. 3.3e-15;
Mismatches 0;
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                                                     Length
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                                                     239;
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  Gaps
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RESULT 10
ABB82743
AC ABB82743
AC ABB82743
AC ABB82
AX ABB82743
AX Caspa
KW human
XX Homo
XX Homo
XX Homo
YX H
   멍
                                                      Qy
                                                                                                                                                                                                                                                                      CC cancer patient. The method involves (a) measuring a level of a tumour up-
CC regulated CARD-containing antagonist of caspase 9 (TUCAN) in a neoplastic
CC cell-containing sample from the cancer patient; and (b) comparing the
CC level of TUCAN in the sample to a reference level of TUCAN, where a low
CC level of TUCAN in the sample correlates with increased survival of the
CC patient. Alternatively, the method involves measuring levels of TUCAN and
CC one or more biomarkers selected from the group of cIAP2, Apafl, Bcl-2, or
CC method is useful for determining a the patient is at risk for relapse,
CC or for determining a proper course of treatment for a patient with
CC cancer. The method is also useful for monitoring the effectiveness of a
CC course of treatment for a patient with cancer, cancer, intended the concer, breast cancer, ovarian cancer, lung cancer.
CC gastrointestinal cancer, melanoma, prostate cancer, or renal cancer. The
CC curse of treatment sequence represents a human Smac polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                      Matches
                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining a prognosis for survival for a cancer patient, useful for determining if the patient is at risk for relapse, comprises measuring a level of TUCAN in a sample from the patient, and comparing it to a reference level -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to determining a prognosis for survival for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; Page 151-153; 153pp; English
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N-PSDB; ABV75367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2;
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                                                                                                                                               Similarity
                                                   AVPIAQKSEPHSLSSEALMRRAVSLVTDST
AVPIAQKSEPHSLSSEALMRRAVSLVTDST
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                                                                                                                                                                                                                                 239 AA;
                                                                                                                   Conservative
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2002US-356934P.
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No. 3
85
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                                                                                                                                            1.3e-1
                                                                                                                                                                       DВ
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                                                                                                                Indels
                                                                                                                                                                    Length
                                                                                                                                                                       239;
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RESULT 11 ABG72301

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Mouse; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepati autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                     Peptide
                                                                                                              Peptide
                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease;
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                          /label= Immuno
/note= "This
137..144
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81..88
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65..72
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97..10
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73..80
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The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids in length. Also included are the polypnocleotide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) with a fragment of the polypeptide, and detecting a reduction in activity of the IAP), producing a natural or synthetic variant of DIABLO
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96.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIABLO; cell death; apoptosis; cancer; vascular disease; her
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
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l; Mismatches
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L.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                             Ota
                                       and/or diagnosis of the full-length cDNAs -
                                                                    Primer sets for sy full-length cDNAs
                                                                                                                                                                                                                                  11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                          (HELI-)
                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                       07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO relational polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO is antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a sample.
                                                                                                                                                                                                                                                                                                           28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB92922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB92922 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, hepatic disease, autoimmune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack, or hepatic tissue damage associated with a liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular dispared by the property of activation of DIABLO, such as cancer, vascular dispared by the property of activation of DIABLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding molecule that specifically binds to DIABLO or its fragmen detecting DIABLO in a biological sample (by contacting the sample with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with cell death activity or which reduces IAP activity,
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                                                                                                                 2001-318749/34.
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                                                                                                                                           Isogai T,
3, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVPIAQKSEPHSLSSEALMRRAVSLYTDST
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27; Conser
                                                                                                                                                                                        HELIX RES INST.
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                                                                    for synthesizing cDNAs defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial
                                                                                                                                                                                                                    2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                           2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence SEQ ID NO:11570.
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                                                                                                                                                                                                                                                               99JP-0248036
99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                         detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                            Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat DIABLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.7%;
                                                                                                                                            hikawa T,
Wakamatsu
                                                     izing polynucleotides, particularly the ed in the specification, and for the det abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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Pred.
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                                                                                                                                            Hayashi K,
A, Nagai I
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No. 4.2e-13;
                                                  the proteins
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                                                                                                                                            Saito K,
Otsuki
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                                                                                                                                                          Yamamoto
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                                                                 detection
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                                                     the
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Claim 8; SEQ

ID 11570; 2537pp + CD

ROM; English

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CC of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                               Novel peptide derived from wild-type human second mitochondria activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human smac (DIABLO) derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB76208 standard;
                  Claim 5;
                                                                                                                                                                                                            13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                           12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                                                                            18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                              WPI; 2002-444169/47.
                                                                                                                                             Fesik SW, Meadows RP,
                                                                                                                                                                                                                                                                                                            WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
             Page 7; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKSEPHSLSSEALMRRAVSLVTDST 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKSEPHSLSSEALMRRAVSLVTDST 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 20
                                                                                                                                                                                                                                                                                                                                       /note= "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
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Pred. No.
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                                                                                                                                             Olejniczak ET,
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RESULT 15
ABP71314
ID ABP71
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ABP71314
ID ABP71
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AC ABP71
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DT 28-AF
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DT 28-AF
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OM1;
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PP 15-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The invention relates to polynucleotides encoding an Omi (serine protease) peptide or polypeptide. The Omi peptide specifically binds to portion of an Inhibitor of Apoptosis Protein (IAP). The Omi polypeptide induces caspase independent apoptosis, or fails to have serine protease activity. The Omi peptides are useful for regulating or altering apoptosis, specifically caspase-mediated apoptosis, and as immunogens for
                                                                                                                                                                                                                                                                                    New Omi nucleic acids and peptides that bind to an inhibitor of apoptosis proteins, useful for regulating or altering caspase-mediated apoptosis and for treating cancer, tumor, or autoimmune diseases \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-2001;
14-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omi; HtrA2; serine protease; inhibitor of apoptosis protein; IAP; caspase; apoptosis; cytostatic; immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-221760/21.
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                                                                                                                                                                                                                            Example 2; Fig 6; 83pp; English.
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immunogens for

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Search completed: October Job time: 78 secs
                                                                                                                                                                     Query Match 49.6
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                            raising antibodies. Enhancers of apoptosis are useful for treating cancers, tumours or for destroying cells that mediate autoimmune diseases. Compositions may also be used for the treatment of diseases associated with inappropriate activation of apoptosis such as neurodegenerative diseases and ischaemic injury. The antibodies can be used in isolating Omi peptides, polypeptides and their variants, in identifying molecules that interact with Omi peptides and polypeptides, and in inhibiting or enhancing the biological activity of Omi peptides and polypeptides. Sequences ABP71310-315 represent fragments of various TAP-binding proteins, used to determine Omi as a IAP-binding protein.
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93.3%; Pred. No. 7.7e-05;
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submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid of A;Reference number: Z18366
A;Accession: T15529

cosmid C17C3

A; Status: preliminary; translated

from GB/EMBL/DDBJ

hypothetical protein C17C3.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t. C;Accession: T15529 R;Du, Z.

20-Sep-1999 #text_change 20-Sep-1999

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A;Description: The sequence of C. elegans cosmid C17C3
A;Reference number: Z18366
A;Accession: T15531
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                             A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-321 <BUZ>
A;Cross-references: EMBL:U41279; NID:g1086905; PID:g1086910; PIDN:AAB52693.1; GSPDB:G
A;Experimental source: strain Bristol N2; clone C17C3
                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T15531
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A; Introns: 45/3; 98/2; 175/2
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A; Experimental source:
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A; Residues: 1-313 < DUZ>
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                                     A; Introns: 16/3; 38/3; 53/3; 106/2; 183/2
                                                         A; Map position:
                                                                           A; Gene: CESP:C17C3.10
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                                                                                               Genetics:
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Query Match
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Best Local :
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12; Conserv
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ce: strain Bristol N2; clone C17C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.6%;
 37.6%; Score 53;
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Pred. No.
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2.3
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Length 321;
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probable membrane protein YMLO23c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 19-Apr-2002
C;Accession: S49754
R;Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: S49741
A;Accession: S49754
A;Cross-references: EMBL:246659; NID:9575680; PID:9575696; GSPDB:GN00013; MIPS:YMLO23c
C;Genetics:
A;Gene: MIPS:YMLO23c
A;Cross-references: SGD:S0004485
A;Cross-references: SGD:S0004485
A;Cross-references: Saccharomyces cerevisiae probable membrane protein YMLO23c
C;Keywords: transmembrane protein
F;61-77/Domain: transmembrane #status predicted <TM1>
F;482-498/Domain: transmembrane #status predicted <TM2>
        RESULT 5
234458
S24458
hypothetical protein R08D7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 19-Feb-1994 *sequence_revision 10-Nov-1995 *tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein slr1888 - Synechocystis sp. (strain PCC 6803)
C. Species: Synechocystis sp.
A. Variety: PCC 6803
C. Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C. Accession: S77148
R. Kaneko, T. Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; A.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada
DNA Res. 3, 109-136, 1996
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                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17706.1; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
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S77148
                                                                                                                                                                                                                                                                                                                                                   A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                            A:Reference number: S74322; MUID:97061201; A:Accession: S77148
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S49754
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13; Conser
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                                                                                                                                                                                                                                                                                                                                               1-630 <KAN>
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12; Conserv
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      #sequence_revision
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41.78;
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6; Mismatches
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Pred. No.
                                                                                                                                                                                                                                              Score 52;
Pred. No.
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10-Nov-1995 #text_change 09-Sep-1997
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5
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Yamada, M.; Yasuda
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elkl protein - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C.Daccession: JC4965; I48339; I48340; S54908
C.Daccession: JC4965; I48339; Jehem, M.; Quatannens, B.; Begue, A.; St
A;Molecule type: mRNA
A;Residues: 1-429 <GRE>
A;Cross-references: EMBL:X87257; NID:g836634; PIDN:CAA60715.1; PID:g836635
A;Experimental source: embyro
R;Giovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, P.; Wasylyk, B.
                                                                                                                                                                                                                                                                                                                                         RESULT 7
JC4965
                                                                                                              A;Title: Structure and organization of the mouse elk1 gene A;Reference number: JC4965; MUID:97017146; PMID:8863747 A;Accession: JC4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: E75401
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A; Residues: 1-256 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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R;Ainscough, R; Hawkins, T.
submitted to the EMBL Datta Library,
A;Reference number: S41036
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A; Residues: 1-455 <AIN>
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Best Local Similarity
Matches 8; Conserv
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38.1%;
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48.1%;
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5.3;
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C;Species: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD2754
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: F20D10.10
C; Superfamily: retroelement pol polyprotein;
F; 146-201/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change :
C:Accession: T05616
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.;
submitted to the protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                     RESULT
AD2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Introns: 70/3; 219/3; 363/3; 397/3
C:Superfamily: elk-1 transforming protein;
F;7-86/Domain: ets DNA-binding domain homol
    A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A; Experimental source: cultivar Columbia;
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A; Residues: 1-720 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z15420
A; Accession: T05616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F20D10.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 23-Sep-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Dev. 8, 1502-1513, 1994
A;Title: Net, a new ets transcription factor that is activated A;Reference number: A53837; MUID:95047310; PMID:7958835
A;Accession: I48339
                                                                                                                                                                                                                                            nitrogen regulation protein nifR [imported] - Agrobacterium tumefaciens (strain
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A; Residues: 1-429 < RES>
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12; Conser
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Pred. No. 18;
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                             tumefaciens C58
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Query Match
Best Local Similarity
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A; Doughty, D.; Scott, C.; Lappas, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                    submitted to the EMBL Data Library, Novembarnescription: The sequence of C. elegans
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B97535
nifr3-like protein [imported] - Agrobacterium tumefaciens (strain C58,
                                       A; Map position: 2
A; Introns: 50/2; 119/2
                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                                                                              C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_rev
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C; Superfamily:
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                                                                          A; Gene: CESP:C17C3.8
                                                                                                            A;Cross-references: EMBL:U41279; NID:g1086905; PID:g1086907; A;Experimental source: strain Bristol N2; clone C17C3
                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-210 < DUZ>
                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                     A; Reference number: Z18366
A; Accession: T15528
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C17C3.8
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A; Residues: 1-338 < KUR>
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A; Status: preliminary
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13; Conserv
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    Caenorhabditis elegans

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Pred. No. 10;
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legans cosmid C17C3
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Length 210;
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                                                                                                                                 PIDN: AAB52692.1;
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A:Description: Genomic sequence for Arabidopsis thaliana
A:Reference number: 214211
A:Accession: T01451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
T01451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 393, 537-544, 1998

A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70663

A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
A:Residues: 1-131 <COL>
A:Cross-references: GB:Z83859; GB:AL123456; NID:g3261678; PIDN:CAB06116.1; PID:g1781209
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv1838C
C:Superfamily: conserved hypothetical protein MJ0974
      phosphate uptake
                                                                                                                                                                                                                                                                                                       A; Introns: 149/3; 301/3
                                                                                                                                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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A; Residues: 1-390 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase homolog F2401.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 1D-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C;Accession: T01451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv1838c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Caccession: F70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 202 E27_21 1000
                                                                                                                                                                                                                                                                                                                                                   A; Gene: ATSP: F2401.13
                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AC003113; NID:g2689438; PID:g2781357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: translated from GB/EMBL/DDB:
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Similarity
13; Conser
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A.Authors: Rerreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; Ge Oliveira, M.C.; de Oliveira, R.C.; Palmiteri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Si
C; Date: 24-Au
C; Accession:
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A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barl.
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fis
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C; Superfamily: DNA-directed DNA polymerase III gamma chain
                                                                                                                                            M.; Tsuhako, M.H.; Vallada, H.; A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004002; GA;Experimental source: strain 9a5c
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A; Residues: 1-608 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;anonymous, The xyre Nature 406, 151-157,
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A;Gene: phoT; SMb21174
A;Genome: plasmid
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A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
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A; Residues: 1-505 < KUR>
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S.; Wells, D.H.; Wong, K.
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33.3%;

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Search Job tim	DЬ	Qy
Search completed: October 2, 2003, 09:40:07 Job time : 45 secs	569 QKSERQQLAEEAFMSDHVVQHLIYQQAAKVVTDS 602	6 QKSEPHSLSSEALM,RRAVSLVTDS 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 2000000000
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_phage:*
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sp_bacteria:*
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O9zigó pseudomonas
Q8dC68 vibrio vuln
O9ruk4 delanococus
Q9szj1 arabidopsis
Q8sy24 arabidopsis
Q9byt9 homo sapien
Q8euz4 mycoplasma
Q8uff3 agrobacteri
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Q9ax95 Oryza sativ
Q18054 caenorhabdi
Q18056 caenorhabdi
Q8df79 vibrio vuln
Q8dd72 vibrio vuln
p73661 synechcyst
Q8avg0 xenopus lae
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Canny Streptococc	OBSA/I Streptococc		40		mus	Q8ixn3 homo sapien	Q9kvk7 vibrio chol	Q9a8q0 caulobacter	Q9st89 oryza sativ	Q8xrd2 ralstonia s	Q9w444 drosophila	Q06344 saccharomyc	Q9pch3 xylella fas	Q8ca49 mus musculu	Q52909 rhizobium m	Q9mav2 arabidopsis	Q8th73 methanosarc	Q8xzx2 ralstonia s	Q8x007 neurospora	Q9hcm6 homo sapien	Q9w696 xenopus lae	Q8p6v8 xanthomonas	Q8pi58 xanthomonas	Q8xyj1 ralstonia s	Q18053 caenorhabdi	Q9xjs5 bacteriopha	Q98mh8 rhizobium l	Q8sv66 encephalito

ALIGNMENTS

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Best Local
         Q9AX95
Q9AX95;
Q1-JUN-2001
01-JUN-2001
01-MAR-2003
P0501G01.22 |
P0501G01.22 |
                                                                                                                                                                                                                                                                                                                                                   Q8R1D8 PRELIMINARY; PRT; 157 AA.
Q8R1D8;
Q08R1D8;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 0610041612 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034780; AAH24780.1; -.
SEQUENCE 157 AA; 17799 MW; OF67319F05EAC6E7 CRC64;
 Oryza sativa
                                                                                                                                                                                                                                                                                                          TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                      54
                                                                                                                                                   1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
|||||||||||| ||| 8
14 AVPIAQKSEPQSLSNEALMRRAVSLVTDST 83
                                                                                                                                                                                                      28;
                                                                                                                                                                                                                   Similarity
                                   1 (TrEMBLrel. 17, 11 (TrEMBLrel. 17, 13) (TrEMBLrel. 23,
                       protein.
                                                                                       PRELIMINARY;
                                                                                                                                                                                                      Conservative
(Rice).
                                                                                                                                                                                                                  92.2%;
93.3%;
                                                              Created)
                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                  Score 130; DB 11;
Pred. No. 2.6e-12;
                                                                                       PRT;
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01-NOV-1996 (TrEMBLrel. 01, Creation of the Control of the
                                                              PROSITE; PS50888; HLH
Hypothetical protein.
SEQUENCE 313 AA; 3
                                                                                                                   TRANSCRIPTION FACTORS.
EMBL; U41279; AAR31421.1;
WormPep; C17C3.7; CE04027.
InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                            Waterston R.;
"Direct Submission.";
"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                          Du Z
"The
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C17C3./.
Caenorhabditis elegans.
Caenorhabditis elegans.
Nematoda;
                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a investigating biology. The C. elegans Sequencinscience 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                   Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q18054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:P0501G01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gramene; Q9AX95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta;
Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                        sequence of C. elegans itted (DEC-1995) to the
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                                                                                                          SM00353; HLH; 1.
    Similarity
12; Conserv
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224 AA; 23798 MW; FEF947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
yta; Magnoliophyta; Liliopsida; Poales; Poaceae;
eae; Oryzea; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nipponbare;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peloderinae;
                                                                                                                                                                                                                                                                                                                                                       N2;
                                                                                         HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9851916;
               37.6%;
                                                              36167
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37.0%;
                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oda; Chromadorea;
Caenorhabditis.
 Score 53; DB Pred. No. 6.1; 3; Mismatches
                                                                                                                                                                                                                                                                                                      cosmid C17C3.";
EMBL/GenBank/DDBJ databases
   ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB
Pred. No. 1.4;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            moto K.;
genomic |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                             DCCE0B2DAC63DF99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEF94A53AE500A92 CRC64;
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Sequencing Consort
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Best Local S
Matches 12
                                                                                                  01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                        Vibrio vulnificus
                                                                        VV10342.
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Q18056;
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01-NOV-1996 (TremBLrel. 01, Cr
01-NOV-1996 (TremBLrel. 01, La
01-MAR-2003 (TremBLrel. 23, La
Hypothetical 37.1 kDa protein.
Ci7C3:10.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
NCBI_TaxID=672;
[1]
                                                                               Cytosine/adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Direct Submission.";
Submitted (SEP-2001) to
-!- SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00010; HLH; 1. SMART; SM00353; HLH; 1
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U41279; AAK31423.1; -
WormPep; C17C3.10; CE04030.
Interpro; IPR001092; HLH_ba
                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a investigating biology. The C. elegans Sequencin Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                             PS50888; HLH_2; 1.
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                                                                                                                                                                                                                                                                                                                                     321 AA;
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                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                Conservative
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                                        Gammaproteobacteria;
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EMBL/GenBank/DDBJ
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Pred. No. 6
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                                                                                             sequence up
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Sequencing Consort
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RESULT 7
p7361
ID 671
ID 7736
AC p736
AC p736
AC p736
DT 01-F
DT 01-W
DE Hypo
GN SLR1
OS Syne
OC Bact
OX NCBI
RN [1]
RP SEQU
RX MEDL
RA MIYAA
RA MASA
RA MASA
RA MASA
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RT TABE
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Best Local S
Matches 10
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01-MAR-2003 (TrEMBLr
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Putative threonine e
VVIII38
                                                   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

REDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.

Kaneko T., Sato S., Kotani H., Tanaka A., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Myajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumu

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumu

Talenichi C.. Wada T., Watanabe A., Yamada M., Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P73661
P73661;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, C
01-FEB-1997 (TrEMBLrel. 02, I
01-MAR-2003 (TrEMBLrel. 23, I
Hypothetical protein slr1888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AE016800; AA009612.1; -
Complete proteome.
SEQUENCE 207 AA; 21859 MW; ADA3B5E7F57E14E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhee J.H., Kim S.Y.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 181 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CMCP6;
                                     Shimpo S., Takeuchi C., Tabata S.;
                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                       SLR1888
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1148;
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      Sequence analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung S.S., Kim J.J., Moon Y.H., Jeong
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Pred. No.
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01-MAY-1999
01-MAY-1999
01-MAR-2003
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Brinkman F.S., Schoofs G., Hancock R.E., De Mot R.;
"Influence of a putative BCF sigma factor on express
outer membrane protein, Optr, in Pseudomonas aerugii
pseudomonas fluorescens.";
J. Bacteriol. 181:4746-4754(1999).
EMBL; AF027290; AAD11567.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to active BCR-related gene.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003702; ActCoA_hydro.
InterPro; IPR000182; GCNSacetyltransf.
Pfam; PF02550; AcetylCoA_hydro; 1.
Pfam; PF005583; Acetyltransf; 1.
Hypothetical protein; Complete proteom
SEQUENCE 630 AA; 70937 MW; 457F681
                                                                                                                                                                                             Bacteria; Proteobacteria; Pseudomonadaceae; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC042307; AAH42307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90908; BAA17706.1; -.
                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                   Putative
                                                                                                                                                                                                                                                                                                                                                         Q9ZIG9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo;
                                                                                                        MEDLINE=99369842; PubMed=10438740;
                                                                                                                            STRAIN-PAO1;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=287;
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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457F6814AFDC7BBD CRC64;
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Matches 10
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01-MAR-2002 (TIEMBLIFEL 20,
Hypothetical protein DR1380.
                                                                                                                                                                                                    MEDLINE=20036896; PubMed=10567266; White O. Elsen J.A., Heidelberg J.F., Hickey E.K., Pet White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Pet Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richar Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zal Makarova K.S., Aravind L., Daly M.J., Minton K.W., Flei
                                   radiodurans Rl.";
Science 286:1571-1577(1999).
EMBL; AE001984; AAF10959.1;
                                                                                                                                                       Ketchum K.A., Nelson
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Deinococcus-Thermus; Deinococcaceae; Deinococcus. NCBI_TaxID=1299;
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01-MAR-2003 (TrEMBLrel. 23, La
01-MAR-2003 (TrEMBLrel. 23, La
Signal transduction histidine
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              DR1380;
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E 928 AA;
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                                                                                                                                                                            nd L.,
K.E.,
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                                                                                                                                                                               K.W., Fleischmann R
h H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                                                                                                                                                                                                                                                           J.D.,
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Q8GYZ4;
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Mayer K.F.)
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Hypothetical 79.2 kDa protein.
F20D10.10 OR AT4G37890.
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EMBL; ALIO35538; CAB37529.1; -.
EMBL; ALIO15538; CAB3754.1; -.
Interpro; IPRO02035; VWF_A.
Interpro; IPRO01841; Znf_ring.
                                                                                                               PROSITE; PS50089; ZF_RING_2; 1.
Hypothetical protein; Metal-binding;
SEQUENCE 720 AA; 79166 MW; 8E910
                                                                                                                                                           SMART; SM00184; RING; SMART; SM00327; VWA; 1
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Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Bevan M., Wedler H., Kutzner M.,

Mayer K.F.X., Schueller C.;

Submitted (FEB-1999) to the EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; SEQUENCE 256 AA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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12; Conser
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            PIAQKSEP------HSLSSEALMRRAVSLVTD
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Kutzner
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the EMBL/GenBank/DDBJ
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Hypothetical protein.
AT4G37890/F20D10_10.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopspermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Tracheophyta;

SEQUENCE FROM N.A.

Ishida

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J., Kawai

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    Q8EUZ4;
01-MAR-2003
01-MAR-2003
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-cv. Columbia;
Seki M., Ilda K., Satou M., Sakurai T., Akiyama K., Ishi
Seki M., Enju A., Kamiya A., Narusaka M., Carninci i
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thallana full-length cDNA ";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKI17301; BAC41972.1; -
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ300461; CAC32454.1;
Genew; HGNC:14004; C11orf25.
Hypothetical protein.
SEQUENCE 981 AA; 114654 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thesis (1996), Department of Human Paris, France.
                                                                                          Q8EUZ4
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Search completed: October Job time: 105 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki Y., Ishikawa J., Yamashita A.,
Yoshino C., Horino A., Shiba T., Sasal
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
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Sasaki T., Hattori M.;
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                                                                                         APPLICANT: Wang, Xiaodong
APPLICANT: Du, Chunying
TITLE OF INVENTION: Activators of Caspases
FILE REFERENCE: UTSD0630
CURRENT APPLICATION NUMBER: US/09/627,393
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 09/479,309
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
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                                     SOFTWARE: Patent
SEQ ID NO 2
LENGTH: 239
TYPE: PRT
ORGANISM: human
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Sequence 2, Application US/09627393 Patent No. 6534267 GENERAL INFORMATION:

Activators of Caspases

Query Match

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TEST	ore 141; ed. No. 1. Mismatches	9-252-991A-3 99-272-991A-2 99-252-991A-2 99-252-991A-2 10-342-648-6 10-34-00198-4 10-34-650-8 19-252-991A-3 19-252-991A-3 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2 19-252-991A-2
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	3 3; 9-15; 0;	US-09-252-991A-31686 US-09-107-532A-5791 US-09-107-532A-5791 US-09-108-648-6 US-09-198-42-648-6 US-09-252-991A-29210 PCT-US94-00198-4 US-09-134-596-7 US-09-134-596-7 US-09-134-596-7 US-09-252-991A-31261 US-09-252-991A-18834 US-09-252-991A-28433 US-09-252-991A-286360 US-09-252-991A-26360 ALIGNMENTS ALIGNMENTS of Caspases //09/479,309
	Len In	
	Length 239; Indels	N N N N N N N N N N N N N N N N N N N
		Sequence
	0;	
	Gaps	31686, 5791, 29621, 7, App 7, App 11, App 11, App 11, App 11, App 26360, 26360,
		91,686, A 991, Appli App
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 30093
LENGTH: 198
     Matches 10; Conserv
                                                                                                                                      SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Applic Patent No. 6225064
                                    Query Match
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                                                                                                                                             TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide FILE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535 CURRENT APPLICATION NUMBER: US 199/413,814 CURRENT FILING DATE: 1999-10-07 EARLIER FILING DATE: 1999-10-07 EARLIER APPLICATION NUMBER: DE 198 46 493.2 EARLIER FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 107 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Matches
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APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                              TYPE: PRT
ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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30; Conserv
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: Brandt, Petra
: Cino, Paul M
                                                                                                                                                                                                                                                                                                        Reichenbach, Hans
                                                                                                                                                                                                                                                                                                                                                       Dougherty, Brian A
Goldberg, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                              Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09413814
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                                                                                                                                                                                                                                                                                                                         Mueller, Joachim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPIAOKSEPHSLSSEALMRRAVSLVTDST 85
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nilarity 33.3%;
Conservative
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pred. No. 88;
mismatches
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Pred. No.
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   Indels
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GENERAL INFORMATION:
APPLICANT: Caboon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB 1169B
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,659
                                                                                                                                                                                                                                                                  ; LENGTH: 799
; TYPE: PRT
; ORGANISM: S.
US-09-165-396-4
US-09-252-991A-24435

: Sequence 24435, Application US/09252991A

: Patent No. 6551795
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Best Local Similarity
Watches 9; Conserve
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US-09-342-648-8
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APPLICANT: BECKER, JEFFREY W.
APPLICANT: LUBKOWITZ, MARK A.
                                                                                                                                                                                           Matches
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                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/165,396
CURRENT FILING DATE: 1998-10-02
EARLIER APPLICATION NUMBER: PCT/US98/02332
EARLIER FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: 60/037,859
EARLIER FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE FILE REFERENCE: 372.6520P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Triticum aestivum
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                                                                                                            58 PESQKFDRHSIQEEGLVWKGDPTYLPNSPYPEVRSAVSIEDDPT 101
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29.5%;
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Best Local Similarity
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                                                                        Matches
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF THE PRIOR FILING DATE: 1998-07-27
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                 TELEFAX: (202)942-8484 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 29-MA CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                              ENGTH:
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109 PSPELQGPPSTEKEAILRRLVALLEE 134
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                                                                                                                                                                                                               amino acid
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                                   PIAQKSEPHSLSSEALMRRAVSLVTD 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                              249 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLO, Gregory J.
VENTION: APOPTOSIS ASSOCIATED PROTEIN BBK
                                                                      Conservative
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)N: 435
                                                                                     30.5%;
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                                                                                     Score 43; DB Pred. No. 29;
                                                                      Mismatches
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                                                                                                     Length 249;
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US-09-188-177-11
                                    ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28715
                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-28715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-09-188-177-11
                                                                                                                                                                                                                                                                                                                                  Sequence 28715, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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Patent No. 6057132
                                                                                           SEQ ID NO 28715
LENGTH: 327
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 1999-02-
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-02-18
                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)942-8484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)942-8459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: WIXON, Henry N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%;
Local Similarity 34.6%;
es 9; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/188,177 FILING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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IVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

IVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202)942-8484
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linear
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30.5%;
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 Score 43;
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Pred. No. 29;
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 DB 4;
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Length 327;
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DB 3;

Length 570; Indels

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Best Local Similarity
Watches 9; Conserve
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-342-648-4
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EARLIER FILING DATE: July 13, 1998
NUMBER OF SEO ID NOS: 10
SOFTWARE: Microsoft Office 97
SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08826246 Patent No. 6048709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILLING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
                     FILING DATE: 16-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHOR
TITLE OF INVENTION: THE TREATMENT AND DIAGN
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
                                                  APPLICATION NUMBER:
                                                                                                                                   CLASSIFICATION:
                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 28-MAR-1997
                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PENNIE & EDMONDS LLP
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                                       16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%;
52.9%;
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Pred. No.
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49;
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                                ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-944-495-2
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US-08-944-495-2
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                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790909
TELEPAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                              TOPOLOGY:
                                                                                          TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                            TELEFAX: (212)8699741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A REGISTRATION NUMBER: 30
                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                          LENGTH:
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10036-2711
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Similarity 43.5%;
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 30.5%;
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Pred. No.
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Score 43;
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Length 570;

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EARLIER FILING DATE: 1996-02-16

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENCTH: 570

TYPE: PRT

ORGANISM: Homo sapiens

US-09-126-640-7
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US-08-925-588-2
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US-09-126-640-7
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Patent NO. 6221628
GENERAL INFORMATION:
APPLICANT: Falb, Dean
APPLICANT: Falb, THE TREATMENT AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FALE, Dean A.
APPLICANT: TALE, Dean A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
FILE REFERENCE: 7853-126
CURRENT APPLICATION UNMBER: US/09/126,640A
CURRENT FILING DATE: 1998-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 08/870,434
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER FILING DATE: 1997-02-13
EARLIER APPLICATION NUMBER: 60/011,787
Local Similarity nes 10; Conserv
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 KSHPEVLIAEALAANAGALITST 473
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STATE: NY
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                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                      ADDRESSEE: PENNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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43.5%;
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4; Mismatches
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SEQUENCE CHARACTERISTICS:
                                                                                                            Local Similarity 43.5 hes 10; Conservative
                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                      451 KSHPEVLIAEALAANAGALITST 473
                                                                                KSEPHSLSSEALMRRAVSLVTDS 29
                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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hypothetical prote
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Oy 15 SEALMRRAVSLVTDS 29 : : : Db	Query Match 24.8%; Score 35; DB 2; Length Best Local Similarity 53.3%; Pred. No. 68; Matches 8; Conservative 3; Mismatches 4; Inde	RESULT 2 151922 151922 Cystic fibrosis transmembrane conductance regulator - rabbit Cyspecies: Oryctolagus cuniculus (domestic rabbit) C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_cha C;Accession: I51922 R;McGrath, S.A.; Basu, A.; Zeitlin, P.L. Am. J. Respir. Cell Mol. Biol. 8, 201-208, 1993 A;Title: Cystic fibrosis gene and protein expression during A;Reference number: I51922; MUID:93152187; PMID:7678968 A;Accession: I51922 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-23 <mcg> A;Cross-references: GB:S54552; NID:9265093; PIDN:AAB25301.1; C;Superfamily: cystic fibrosis transmembrane conductance reg</mcg>	Ouery Match Best Local Similarity 53.3%; Pred. No. 58; Matches 8; Conservative 3; Mismatches 4; Inde Oy 6 OKSEPHSLSSEALMR 20 : :	RESULT 1 T48881 leader peptide [imported] - Vibrio sp. C;Species: Vibrio sp. C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change C;Accession: T48881 R;Xu, Y, Zhang, Y, Liang, Z.Y.; Van de Casteele, M.; Legrain, Microbiology 144, 1435-1441, 1998 A;Title: Aspartate carbamoyltransferase from a psychrophilic de A;Reference number: Z24845 A;Reference number: Z24845 A;Accession: T4881 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-20 <xuy> A;Experimental source: StMBL:Y09786; PIDN:CAA70922.1 A;Experimental source: Strain 2693</xuy>	ALIGNMENTS	30 25 17.7 29 2 B61613 31 25 17.7 30 2 S07217 32 24.5 17.4 23 2 A59480 33 24.5 17.4 25 2 PC4445 34 24 17.0 12 1 A43975 35 24 17.0 18 2 S55002 37 24 17.0 20 2 H28949 38 24 17.0 21 2 A59486 39 24 17.0 21 2 A59325 40 27 17.0 25 2 PO0369 41 24 17.0 25 2 PO0369 41 24 17.0 25 2 PO0369 41 24 17.0 25 2 D20554 43 24 17.0 25 2 D20554 43 24 17.0 26 2 H24743 44 17.0 26 2 H24743 45 24 17.0 26 2 H24753 46 27 113836
	gth 23; Indels 0; Gaps 0;	bbit (fragment) _change 20-Aug-1999 . ing fetal lung development. 1.1; PID:g265094 regulator; ATP-binding casse	gth 20; Indels 0; Gaps 0;	t_change 02-Jun-2000 Legrain, C.; Glansdorff, N. hilic deep-sea bacterium, Vibr		ceratotoxin B - Me ribosomal protein NADP phosphatase I L-ascorbate peroxi locustamyotropin - hypothetical prote protein l - Legion ribosomal protein mast cell proteina probable bacteriop L protein - rabies cytotoxic T-lympho hemocyanin subunit prolactin, 24K - M interferon alpha (NADH2 dehydrogenas

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class I histocompatibility antigen H-2K(d) alpha chain, alternate splice form C; Species: Mus musculus (house mouse)
C; Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 07-May-1999
C; Accession: A60897
R; Abu-Hadid, M.M.; Fuji, H.; Sood, A.K.
Mol. Immunol. 25, 739-749, 1988
A; Title: Identification of an alternatively spliced K(d) and the Qa-6(d) mRNAs A; Reference number: A60897; MUID:89039921; PMID:3141798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Primary structure of the site on bovine hormone-sensitive lipase phosphorylated A; Reference number: $00347; MUID:88152238; PMID:3345839
A; Recession: $00347
A; Rolecule type: protein
A; Residues: 1-27 <GAR>
C: Comment: Activation of this enzyme involves phosphorylation of Ser-8 by cyclic AMP-dep C: Superfamily: hormone-sensitive lipase C: Keywords: carboxylic ester hydrolase; lipid degradation: phosphoprotein F:8/Binding site: phosphate (Ser) (covalent) #status experimental F:10/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-20 <ABU>
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A60897
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$00347

triacylglycerol lipase (EC 3.1.1.3) - bovine (fragment)

N;Alternate names: hormone-sensitive lipase
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: $00347
R;Garton, A.J.; Campbell, D.G.; Cohen, P.; Yeaman, S.J.
FEBS Lett. 229, 68-72, 1988
FFBS Lett. 229, 68-72, 1988
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Mol. Gen. Genet. 210, 490-497, 1987
A;Title: Expression of leucine genes from an extremely thermophilic
A;Reference number: S00901; MUID:88121725; PMID:3323845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leu leader peptide - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S00901
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A; Residues: 1-15 <CRO>
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Pred. No. 2.4e+02
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C; Date: 17. [C] Accession: A60728
C; Accession: A60728
R; Pineau, T.; Galtler, P.; Bonfils, C.; Derancourt, J.; I
Blochem. Pharmacol. 39, 901-909, 1990
A; Title: Purification of a sheep liver cytochrome P-450
A; Title: Purification of By MUID: 90179800; PMID: 2310415
                                                                                                                                                                                                                                                  RESULT 8
A60728
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(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
(;Accession: G42753
R;Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.;
J. Biol. Chem. 267, 15210-15216, 1992
A;Title: Purification and characterization of multiple components of human lymphoblas
A;Reference number: A42753; MUID:92340576; PMID:1634550
A;Accession: G42753
                                                                                                                                                              C;Species: Ovis sp. (sheep)
C;Date: 14-May-1993 #sequence_revision 14-May-1993
                                                                                                                                                                                                     cytochrome P450 3A, troleandomycin-induced - N; Contains: oxidoreductase (EC 1.-.-)
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C; Keywords: ele
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Arch. Biochem. Biophys. 271, 284-299, 1989
A;Title: Characterization of a phenobarbital-inducible (A;Reference number: S04341; MUID:89271912; PMID:2786372
A;Accession: S04341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CYP3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Canis lupus familiaris (dog)
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Best Local
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8; Conserv
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: protein
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of multiple components of human lymphoblas {\tt PMID:}1634550
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8.9e+02;
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                                                                                                                                                            #text_change 05-Mar-1999
                                                                                                                       J.; Maurel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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                                                                             from the P450IIIA gene
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P450 isozyme is a member of the P450IIIA family

but

is not

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RESULT
A30323
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Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthal A;Reference number: A48186; MUID:93317598; PMID:8327463
A;Accession: A48186
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C48186
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C;Genetics:
A;Gene: CYP3A
C;Superfamily: human cytoch
C;Keywords: electron transf
amyloid protein AL (Ig lambda chain V region) - human (fragment) C;Species: Homo sapiens (man) C;Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change C;Accession: A30323
                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-23 <DE1>
A; Experimental source: pollen
A; Note: sequence extracted fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A48186
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A48186
ATP synthase beta-1 chain - wood tobacco (fragment)
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A;Title: Specific mitochondrial proteins in pollen: presence A;Reference number: A48186; MUID:93317598; PMID:8327463
A;Accession: C48186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPase R1 subunit - wood tobacco (fragment)
C:Species: Nicotiana sylvestris (wood tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C:Accession: C48186
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nes 6; Conserv
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nes 6; Conserv
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46.78;
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               21-Feb-1990 #text_change 16-Aug-1996
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le+03;
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heme; monooxygenase;
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RESULT 13
A37825
                                                                                                                                                                                                                                                       fibronectin receptor alpha chain - chicken (fragment)
c;Species: Gallus gallus (chicken)
c;Decies: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 18-Jun-1993
C;Accession: A37825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 2. Page 1. The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein K09E3.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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T29626
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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                           Qy
                                                                                                                           A; Molecule type:

a Residues: 1-24
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                                                                                                                                                                                          A; Title: Identification and characterization of a dimeric chicken fibronectin recepto A; Reference number: A37825; MUID:90354452; PMID:2143763
                                                                                                                                                                                                                         R;Hofer, U.; Syfrig, J.; Chiquet-Ehrismann, J. Biol. Chem. 265, 14561-14565, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Clin.
                                                                                                                                                             A; Status: preliminary
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5 TQPHSVS 11
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PFAFRGSPGSLFGFAL
                              PIAQKSEPHSLSSEAL 18
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                                                                                                                               protein <HOF>
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                                                              Conservative
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57.1%;
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                                                                            Score 26;
Pred. No. 1
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Pred. No. 1
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Pred. No. 1.4e+03;
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legans cosmid
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1.8e+03;
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1.8e+03;
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RESULT 14

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cytochrome P450 Htp3 - human (fragment)
N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C;Catces: Homo sapiens (man)
C;Cotes: Homo sapiens
C;Cotes: 
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Hu-like protein HB1 - Bifidobacterium longum (fragment)
C.Species: Bifidobacterium longum
C.Species: Bifidobacterium longum
C.Species: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 16-Feb-1997
C.Accession: A43768
R.Goshima, N.; Kano, Y.; Imamoto, F.
Biochimie 72, 207-212, 1990
A.;Hitle: Characterization of HU-like protein from Bifidobacterium longum.
A.Reference number: A43768
A.;Accession: A43768
A.;Status: preliminary
A.;Molecule type: protein
A.;Residues: 1-27 <GOS>
C.;Keywords: DNA binding
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Search completed: October 2, 2003, 09:43:21 Job time : 19 secs
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COG1_CHIOP
DER6_DERFT
SCB1_CANPA
CH60_BOVIN
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RESI ID AC AC DT DT DT DT DT DT OC OC	Oy Ma	SQ SQ	88888888	8888	RRRRR	ROC	1888		RESI LPL ID		
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Bur. J. Biochem. 179:249-254(1989).

-i. Function: In Adipose Tissue and heart, It primarily hydrolyzes
STORED TRIGUCERIDES TO FREE PATTY ACIDS, WHILE IN STEROIDGENIC
TISSUES, IT PRINCIPALLY CONVERTS CHOLESTERYL ESTERS TO FREE
CHOLESTEROL FOR STEROID HORMONE PRODUCTION.

-i. ENAYME REGULATION. RAPIDLY ACTIVATED BY CAMP-DEPENDENT
PHOSPHORYLATION UNDER THE INFLUENCE OF CATECHOLAMINES.

-i. PATHWAY: HORMONE SENSITIVE LIPASE CATTALYZES THE RATE LIMITING
STEP IN TRIGLYCERIDE LIPOLYSIS.

-i. STMILARITY: BELONGS TO THE "COV". -..
                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
20 kDa neutrophil cationic protein (NC
sus scrofa (Plg).
                                                                                                                                                                                                                                                    NCP_PIG
P80552;
                                                                                 Fornhem C., Peterson C.G.B., Alving "Isolation and characterization of granule proteins.";
                                                  SEQUENCE
                                                                                                                     MEDLINE=96242065;
                                                                                                                                   SEQUENCE
                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garton A.J., Campbell D.G., Cohen P., Yeaman S.J.; "Primary structure of the site on bovine hormone-sensitive lipase phosphorylated by cyclic AMP-dependent protein kinase."; FEBS Lett. 229:68-72(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garton A.J., Campbell D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 8-12, AND PHOSPHORYLATION OF SER-10 TISSUE-Adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP-activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89137090; PubMed=2537200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation of bovine hormone-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keaman S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88152238; PubMed=3345839;
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             Local
                                                        Arch. Allergy
CER 25
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11; Conserv
  Similarity 6; Conserv
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PS01174; LIPASE_GDXG_SER; PARTIAL.
                                                                                                                                                                                                                                                                                                                        KTEPMRRSVSEAALTQPEGPLGTDS
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  Conservative
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                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                      PubMed=8645990;
son C.G.B., Alvi
                                                               Immunol.
                                                2629 MW;
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           20.6%;
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27
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44.0%;
  4;
Score 29; DB
Pred. No. 3.1e
4; Mismatches
                                                                     110:132-142(1996)
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                                              5275BFFF8D81F3AD CRC64;
                                                                                                       Alving K.;
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                       DB 1;
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.2e+02;
9;
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(BY
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Gaps
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RESULT 4
UP35_UP AU
UP35_U
ID UP35_U
AC P82042
DT 30-MAY
DT 11-MAY
KW Amphit
FT MOD_RE
SO SEQUEN
RESULT 5
FOR1_MYRGU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                           TISSUE=Hemolymph;

MEDLINE=98165787; PubMed=9497332;

Mackintosh J.A., Veal D.A., Beattie A.J.,

"Isolation from an ant Myrmecia gulosa of
0-glycosylated proline-rich antibacterial
0-glycosylated proline-rich antibacterial
J. Biol. Chem. 273:6639-6143(1998).
                                                                                                                                                                                                                                                                 Myrmecia gilosa (Red bulldog ant).
Myrmecia gilosa (Red bulldog ant).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UP35_UPEMJ
P82042;
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15-DEC-1998 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
"New antiblotic uperin peptides from the dorsal glands of the australian toadlet Uperoleia mjobergii.";
aust. J. Chem. 49:1325-1331(1996).
                                         -!- INDUCTION: By bacterial infection.
-!- PTM: O-LINKED GLYCAN CONSISTS OF A
                                                                                                                                                                                                               SEQUENCE, AND CARBOHYDRATE-LINKAGE
                                                                                                                                                                                                                                            NCBI_TaxID=36170;
                                                                                                                                                                                                                                                            Myrmeciinae; Myrmecia.
                                                                                                                                                                                                                                                                                                                          Formaecin 1.
                                                                                                                                                                                                                                                                                                                                                                     P81438;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: Expressed by the si-i- MASS SPECTROMETRY: MM=1779; METHOD=FAB Amphibian defense peptide; Antibiotic; Amio MOD_RES 17 17 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uperoleia mjobergii (Australian toadlet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                                                                                                                                                                     FOR1_MYRGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia;
Myobatrachinae; Upero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uperin 3.5.
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30-MAY-2000 (Rel.
15-SEP-2003 (Rel.
         PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY. SIMILARITY: TO DROSOPHILA DROSOCIN.
                                                                                      FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.INNOCUA, M.LUTEUS, S.AUREUS, P.MULTOCI, S.EPIDERMIS AN
                                                                          BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LMRRAVSLV
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(Rel. 39, Last seq
(Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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39,
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Last annotation updat
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1; Mismatches
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2.8e+02;
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                                                                                                                                two inducible
peptides.";
                                                                                                                                                                 Gooley A.A.;
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Antibiotic;

Glycoprotein;

Insect

immunity; Hemolymph

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RESULT 6
ATPA_BRYMA
ID ATPA_B
AC P26965
DT 01-AUG
CC Eukary
OC Buxary
OC ATPA.

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RN [1]
RP SEQUEN
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01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
15-SEP-2003 (Rel. 4
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONO M., Satoh H., Okabe Y., Abe Y., Nakayama K., Okada M.;
"Nucleotide sequence of the large subunit of
ribulose-1,5-bisphosphate carboxylase/oxygenase from the green alga
Bryopsis maxima.";
plant Mol maxima.";
                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                             PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL. ATP synthesis; Chloroplast; Thylakoid; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol. Biol. 17:505-508(1991).
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                                                                                                                                                                                                                                      ATP-binding; Hydrolase; Hydrogen ion
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                                                                                                                                                                                                                                                                                                                InterPro; IPR000194; ATPase_a/bcentre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H(+)(Out).

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATAL SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATAL CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FI SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1): HAS THREE MAIN SUBUNITS: A, B AND C.

SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.

SIMILARITY: Belongs to the ATPASE alpha/beta chains family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP +
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                                                                                                                                                                                                                                                                                                                                            S17432;
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IIMSTNTFSEEAEALLKEAL 21
                                        IAQKSEPHSLSSEALMRRAV 23
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23; Last sequence update)
42, Last annotation update)
a chain (EC 3.6.3.14) (Fragment).
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44.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlorophyta; Ulvophyceae; Caulerpales;
                                                                                           Score 26; DB Pred. No. 1.165; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26;
Pred. No.
                                                                                                                                                                                           A25A0BAD077F338B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O-LINKED (GALNAC. . .).
80CEA3AABBC2EOAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 COMPONENTS, CF(1) - THE CATALYTIC ANE PROTON CHANNEL. CF(1) HAS FIVE
                                                                                                                                                                                                                                      transport.
                                                                                   1.1e+03;
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                      Length 29;
                                                                                                                                                                                                                                                                CF(1);
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(1). CF(0)
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RESULT 8
SODE_PASPI
ID SODE_P
AC P81527
DT 15-DEC
DT 15-DEC
DT 28-FEB
DE SUBERO
GN SODB.
OS PASTEU
OC BACTER
OC VIBRIO
OX NUBRIT
RN MEDLIN
RX MEDLIN
RX MEDLIN
RA BARNES
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Best Local
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NON_TER
SEQUENCE
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P81527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Expression of the putative Duchenne muscular dystrophy gene differentiated myogenic cell cultures and in the brain."; Nature 331:635-638(1988).
 STRAIN=MT1415;
MEDLINE=99173752;
Barnes A.C., Bale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P11530;
01-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMD_RAT
                                                                   Vibrionaceae; Pho
NCBI_TaxID=38294;
                                                                                            Pasteurella piscicida (Photobacterium damsela (subsp. piscicida)). Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003
                                           SEQUENCE.
                                                                                                                                     Superoxide
                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-88122671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Interacts with the syntrophins SNTA1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S01614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X07000; CAA30057.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01614; S01614. Actbind_actnin.
ro; IPR001509; ww_msp5_wwp.
ro; IPR001202; ww_msp5_wwp.
E; PS00019; ACTININ_1; PARTIAL.
E; PS00020; ACTININ_2; PARTIAL.
E; PS01159; ww_DOMAIN_1; PARTIAL.
E; PS01159; ww_DOMAIN_2; PARTIAL.
                                                                                                                                                                                                                                                                        11 RKLQDASRSAQALVEQMVN
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                                                                                                                                     dismutase
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(Rel. 12, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                            Conservative
  Balebona
                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                  Photobacterium
                                                                                                                                                                                                     STANDARD;
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PubMed=10075430;
oona M.C., Horne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=3340214;
                                                                                                                                                                                                                                                                                                                                                                                29
3289 MW;
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                                                                                                                                                                                                                                                                                                                                      18.4%;
31.6%;
                                                                                                                                  Last sequence update)
Last annotation update)
[Fe] (EC 1.15.1.1) (Fragment).
                                                                                                                                                                             Created)
    Horne M.T.,
                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No.
                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                8ECFB28A1A7ACAF0 CRC64;
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                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                         1.1e+03
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    Ellis A.E.;
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RESULT 10
RECX_AZOVI
ID RECX_A
AC P37863
DT 01-OCT
DT 01-OCT
DT 28-FEB
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                                                                                                                                                           Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                    STRAIN-CV. Golden Harvest, and CV. Prof. Blaau MEDLINE-941/1801; PubMed=8125993;
MO H., Van Damme E.J.M., Peumans W.J., Goldste "Isolation and characterization of an N-acetyl-D-galactosamine-binding lectin from D recognizes the blood group A disaccharide (Gal. J. Biol. Chem. 269:7666-7673(1994).

-1- FUNCTION: GAL / GALNAC-SPECIFIC LECTIN. AGAND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUTRESPECTIVE OF BLOOD GROUP TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
P37863;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
N-acetyl-D-galactosamine-binding lectin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                       binding lectin subunit B) (Fragment). Iris hollandica (Dutch iris). Eukaryota; Viridiplantae; Streptophyta;
                                                  RECX_AZOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
-!- COFACTOR: Iron.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic.
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRIHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Iron; NON_TER 20 2
                                                                                                                                                                                                                                    lectin
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=35876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LECB_IRIHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00081; sodfe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Superoxide dismutase and cat piscicida and their roles in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 145:483-494(1999).
                                                                                                                                                                                                                                               SUBUNIT: DISULFIDE-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO
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6; Conserv
                                                                                                                                                           Similarity
5; Conserv
                                                                                                            LSEETMMR
                                                                                                                                   LSSEALMR 20
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                                                                                                                                                                                                          20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                  STANDARD;
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2246 MW;
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                                                                                                                                                                       17.7%;
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50.0%;
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  Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and catalase in Photobacterium damselae subsp.
ples in resistance to reactive oxygen species.";
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THE IRON/MANGANESE
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Pred.
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                                                                                                                                                                                                          DE08DA025FD17D56 CRC64;
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                              Liliopsida;
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2;
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BUT NOT HUMAN
                                                                                                                                                                                                                                                                                                       Dutch Iris bulbs which alNAc alpha 1-3Gal).";
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                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                          I.J.;
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bulb
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RESULT
ALL7_OL
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Best Local
                                                                       Tejera M.L., Vilialba M., Batanero E., Rodriquez R.;
"Identification, isolation, and characterization of Ole e
allergen of olive tree pollen.";
J. Allergy Clin. Immunol. 104:797-802(1999).
                                                                                                                                                                                                                                                                        ALL7_OLEEU STANDARD; PRT; 21 AA. P81430; 30-MAY-2000 (Rel. 39, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Pollen allergen Ole e 7 (Ole e VII) (Fragment).
                                                                                                                                                              SEQUENCE (VARIANTS A AND B), TISSUE=Pollen;
                                                                                                                                                                                                                    Olea europaea (Common olive).
Eukaryota; Viridiplantae; Etteptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Lamiales; Oleaceae; Olea.
                                                                                                                                              MEDLINE=99449676;
                                                                                                                                                                                                                                                                                                                                                                      OLEEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                        NCBI_TaxID=4146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_01114; -;
NON_TER 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 22:1313-1314(1994).
-!- FUNCTION: Modulates recA activity (By similarity).
-!- SUBCELULUAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE RECX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Mot R., Schoofs G., Vanderleyden J.,
"A putative regulatory gene downstream
"A putative and Gram-positive bacteria.";
m::0146 Por 20:1117-111411004."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S96898; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 113:47-53(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venkatesh T.V., Das H.K.;
"The Azotobacter vinelandii recA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulatory RECX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94218258; PubMed=8165147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation of expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92225347; PubMed=1563632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION
POLYMORPHISM: Many isoforms of the allergen exist due to polymorphism. They can be classified as isoforms of type A (showners) and isoforms of type B. A microheterogeneity is detected a positions 4 and 11 of isoforms of type B.

MISCELLANEOUS: Allergen from olive pollen. Important in
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LSSEALMRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               LDSPAAVRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein recX (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                PubMed=10518824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azotobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25;
Pred. No.
                                                                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C809F8BCCED6CB56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene:
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                                                                                                                                                                                                                                     eudicots
                                                                                                                                                                                                                                                Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions on
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                                                                                                                   7,
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L outstation -
                                                        (shown
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allergen; Polymorphism.
VARIANT 5 5
VARIANT 10 10
VARIANT 18 18
NON TER 21 21
                                                                                                                                                                                                                                    Enterococcus faecalis.",
Enterococcus faecalis.",
Science 299:2071-2074(2003).

Science 299:2071-2074(2003).

-i- FUNCTION: ACTS AS A COMPETITIVE INHIBITOR OF THE

-i- SUBCELLULAR LOCATION: Secreted (Probable).

-i- MISCELLANEOUS: IAD1 APPEARS TO BE A COMPONENT OF
                                                                                                                                                                                                                                                                                                          Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W., Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _ENTFA
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91261999; PubMed-2128961;
Clewell D.B., Pontius L.T., An F.Y., Ike Y., Suzuki A., Nakayama
"Nucleotide sequence of the sex pheromone inhibitor (iAD1)
determinant of Enterococcus faecalis conjugative plasmid pAD1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
 CHAIN
SEQUENCE
                                                      TIGR;
                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-V583 / ATCC 700802; PLASMID-pTEF1; MEDLINE-22550857; PubMed-12663927;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid 24:156-161(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pTEF1, and Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAD OR EFA0005.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sex pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P24803;
                                                                 PIR; A37391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAD1_ENTFA
                             PROPEP
                                         Plasmid.
                                                                                           EMBL; M62888; AAA98039.1;
                                                                                                                                                                                                                                 SEQUENCE.
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6; Conserv
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 22 AA;
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18
21
AA;
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                                                                                AAO83007.1;
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POTENTIAL.

SEX PHEROMONE INHIBITOR DETERMINANT DOEAEBDF1BCD9D08 CRC64;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California. Its prevalence is related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           × × 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor
                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1e+03;
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TYPE
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                                                                                                                                                                                                                                            ITS OWN SIGNAL
                                                                                                                                                                                                                                                                       CAD1 PHEROMONE
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CHOLLEY 13
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                                                                                                                                                                                                                                                                                      RESULT 14
CERB_CERCA
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                        01-JUN-1994
01-JUN-1994
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chaperone;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a chaperonin in a moth, Heliothis virescens.";
J. Mol. Biol. 214:407-422(1990).
1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND
MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF
IMPORTED PROTEINS. MAY ALSO PREVENT MISPOLDING AND PROMOTE THE
REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
Eukaryota; Metazoa; Arthropoda; Hexa
Neoptera; Endopterygota; Diptera; Br
Tephritoidea; Tephritidae; Ceratitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90339485; PubMed=1974308;
Miller S.G., Leclerc R.F., Erdos G.W.;
"Identification and characterization of a testis-specific isoform of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heliothis virescens (Noctuid moth) (Owlet moth),
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
60 kDa chaperonin, mitochondrial (P60) (Fragm
                                                                                                                                                                                                                                   CERB_CERCA
P36191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P26317;
                                                                             Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                   Ceratotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001844; Chaprnin_Cpn60.
PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH60_HELVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the chaperonin (HSP60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL SIMILARITY).

SIBUNIT: FORMS A SINGLE SEVEN-MEMBER RING COLASSOCIATION WITH THE P63 PROTEIN.

SUBCELLULAR LOCATION: Mitochondrial.

TISSUE SPECIFICITY: Testis.

DEVELOPMENTAL STAGE: FROM THE SECOND HALF OF INSTAR, THROUGH THE FIRST TWO DAYS OF PUPAL!

MISCELLANEOUS: SHOWS ATPASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ALMRRAVSLVTDS 29
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                                                                                                                                                                                                                                                                                                                                                                                               ALMLQGVDVLADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Testis; Mitochondrion
                                                                                                                                                      (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AA;
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                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                        29, Created)29, Last sequence up33, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2531 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.7%;
38.5%;
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30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN THE MITOCHONDRIAL MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2B34508F8CA981CF CRC64;
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                                                     Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                          Brachycera;
                                                                                                                                                                                   update)
                                                                                                                                                           update)
                                                                                                                                                                                                                                                              29
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MEDLINE=79045279; PubMed=152199;

MEDLINE=79045279; PubMed=152199;

MITCH N., Willick G., Nazar R.N.;

Smith N., Watheson A.T., Yaguchi M., Willick G., Nazar R.N.;

The 5-S RNA-protein complex from an extreme halophile,

Halobacterium cutirubrum. Purification and characterization.";

Eur. J. Biochem. 89:501-509(1978).

LIST SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        P05970;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
50S ribosomal protein L18P (HCUL18) (HL13) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marchini D., Giordano P.C., Amons R., Bernini L.F., Dallai R.;

"Purification and primary structure of ceratotoxin A and B, two
antibacterial peptides from the female reproductive accessory glands
of the medfly Ceratitis capitata (Insecta:Diptera).";
Insect Biochem. Mol. Biol. 23:591-598(1993)

-i- FUNCTION: FEMALE-SPECIFIC PEPTIDES WITH POTENT ACTIVITY AGAINST
GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. THEY HAVE AS WELL
HEMOLYTIC ACTIVITY. THESE PROTEINS ARE STABLE EVEN AT 100 DEGREES
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Halobacteriaceae; Halobacterium.
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MEDLINE=93357786; PubMed=8353519;
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SUBUNIT: HOMOPOLYMER OF FOUR TO SIX SUBUNITS.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: STRUCTURALLY RELATED TO CECROPINS, DEFENSINS AND
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FE 29 AA; 2861 MW; EE57F4EECB2DA6B0 CRC64;
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Q2939 oryctolagus
O57546 lampetra pl
Q9jmv3 escherichia
Q8ia94 caenorhabdi
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Q8clal yersinia pe
Q9r4w6 helicobacte
O57547 lampetra pl
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01-MAY-1997 (TEMBLrel. 03, L
01-DEC-2001 (TEMBLrel. 19, L
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Vibrio sp. (strain 2693).

Bacteria; Proteobacteria; G

Vibrionaceae; Vibrio.

NCBI_TaxID=79682;
Q29399 PRELIMINARY;
Q29399;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                   "Aspartate carbamoyltransferase from a psychrophilic deep-sea bacterium, Vibrio strain 2693: properties of the enzyme, genetic organization and synthesis in Escherichia coli."; Microbiology 144:1435-1441(1998).

EMBL; Y09786; CAA70922.1; -.

SEQUENCE 20 AA; 2241 MW; 35C31F588FBB5D63 CRC64;
                                                                                                                                                                                                                                                                                                                                  MEDLINE=98274751; PubMed=9611817; Xu Y., Zhang Y., Liang Z.Y., Van de Casteele M., Legrain Glansdorff N.;
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8; Conserv
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01-OCT-2000 (TremBLrel.
01-JUN-2002 (TremBLrel.
             Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Homeobox protein LpHox4-7A (Fragment).
Lampetra planeri (Brook lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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NCBI_TaxID=562;
                                                                                                        Luciferase
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MEDLINE=98358009; PubMed=9694633;
Sharman A.C., Holland P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Estimation of Hox gene cluster number Int. J. Dev. Biol. 42:617-620(1998). EMBL: AF044802; AAC03006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petromyzontiformes; Petromyzontidae; Lampetra. NCBI_TaxID=7750;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolag
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Cystic fibrosis transmembrane conductance regulator
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Bristol N2;
STRAIN-Bristol N2;
Madsen C., Kalicki J., Yoakum
"The sequence of C. elegans cc
"The sequence of Mar-2001) to the El
                                                       Waterston R.; Submitted (DEC-2002) to the EMBL; AC090999; AAO12396.1;
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SEQUENCE FROM |
STRAIN=HB101;
   Hypothetical protein SEQUENCE 30 AA; 3
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                 STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
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Olsson O., Koncz C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
56 kDa major heat shock protein (Fragment).
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                    Yokota K., Hirai Y., Haque M., Hayashi S., Isogai H., Nagamahi E., Tsukada Y., Fujii N., Oguma K., "Heat shock protein produced by Helicobacter pylori."; Microbiol. Immunol. 38:403-405(1994).

SEQUENCE 20 AA; 2326 MW; 995EEETC51529BAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SPONIENCE 30 AA; 3461 MW;
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EMBL; AE013778; AAM85323.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE-22137863; PubMed-12142430;
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Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Yersinia.
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Y1754.
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01-MAR-2003
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NCBI_TaxID=210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
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Pred. No. 8.
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Pred. No. 9e+02;
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Pred. No. 6.3e+02;
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Q8WXC8;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HOMEODOX protein LpHOx4-7B (Fragment).
Lampetra planeri (Brook lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontiformes; Petromyzontidae; Lampetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 111:931-939(1996).
HSSP; P06139; 1AON.
SEQUENCE 30 AA; 3233 MW; AF5A
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01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
Heat shock protein 60 (Fregment).
Narcissus pseudonarcissus (Daffodil).
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Q9T2P9;
01-MAY-2000 (TrEMBLrel.
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MEDLINE=98358009; PubMed=96
Sharman A.C., Holland P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonk M., Tadros M., Vandekerckhove J., Al-Babili S., Beyer P., "Purification and characterization of chaperonin 60 and heat-sprotein 70 from chromoplasts of Narcissus pseudonarcissus.";
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Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidac
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Homo sapiens (Human).
Homo sapiens (Human).
'harvota; Metazoa; Chordata; 'haria; Primates;
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Lamba J.K., Adachi M.,
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"Transcription Factors NF-Y and Promoter Activity of the Bovine
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O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome c oxidase subunit II (Fragment).
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Pfam; PF00116; COX2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 based on mitochondrial sequence data.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AF188441; AAG12284.1;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ database EMBL; AF168437; AAG12279.1;
InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PF00116; COX2; 1.
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NCBI_TaxID=135985;
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[ (TrembLrel. 16, CrembLrel. 16, Later of the CrembLrel. 22, Later of coxidase subunit ]
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ian white-eyes
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SILKAS B., Jones I.B., Derrickson S.R., Fleischer R.C.;

Silkas B., Jones I.B., Derrickson S.R., Fleischer R.C.;

"Phylogenetic relationships of Micronesian white-eyes (Zosteropidae) based on mitochondrial sequence data.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF168434; AAG12275.1; -

EMBL; AF168434; AAG12275.1; -

InterPro; IPR001429; Cyt_c_ox_2.

Pfam; PF00116; COX2; 1.

Oxidoreductase; Mitochondrion.
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Q9GB45;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome c oxidase subunit II (Fragment).
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Slikas B., Jones I.B., Derrickson S.R., Fleischer R.C.;

"Phylogenetic relationships of Micronesian white-eyes (Zosteropidae)

based on microchondrial sequence data.";
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Pred. No. 2.4e+03;
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-039-642B-5
US-10-053-485-3
US-09-579-664B-27
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US-08-135-166-47
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102, Appl

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102, Appl

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102, Appl

103, Appl

104, Appl

105, Appl

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107, Appl

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Sequence 46, Appl	Sequence 3, Appli	Sequence 21, Appl	Sequence 43, Appl	Sequence 150, App	Sequence 668, App	Sequence 36, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 806, App	Sequence 56, Appl	Sequence 56, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl		

ALIGNMENTS

US-08-755-587-216 RESULT 1 US-08-755-587-216 ...real, Phillip A ...realCANT: Wooster, Richard F applicaNT: Ashworth, Alan ApplicaNT: Stratton, Michael R TITLE OF INVENTION: Materials and TITLE OF INVENTION: identification TITLE OF INVENTION: Suscention NUMBER OF SECTION: Query Match Best Local S Matches 9 Sequence 21 Patent No. APPLICATION NUMBER: GB 9525555.0 ETILING DATE: 14-DEC-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9617961.9 ETILING DATE: 28-AUG-1996 ATTORNEY/AGENT INFORMATION: NAME: Kenneth D Sibley REGISTRATION NUMBER: 31,665 REFERENCE/DOCKET NUMBER: 5405-135 INFORMATION FOR SEQ ID NO: 216: APPLICATION NUMBER: GB 9 FILING DATE: 23-NOV-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/755,587 FILING DATE: 25-NOV-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9523959.6 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentl STREET: 310 UC CITY: Raleigh LENGTH: 26 amino acids TYPE: amino acid ADDRESSEE: TOPOLOGY: 16, Application US/08755587 6045997 Similarity 9; Conserv NO USA 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107 IBM PC compatible SYSTEM: PC-DOS/MS-DOS Bel1 Seltzer Park & Gibson Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof. 23.8%; Release #1.0, Score 33.5; D Pred. No. 59; 5; Mismatches Version #1.25 DВ ω Length 26; (EPO)

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US-08-306-078-3
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US-08-031-148-6
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                                                                                                                                                                   Sequence 3, Application US/08306078 Patent No. 5827646
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                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                      APPLICANT: van Grunsven, Wouterus Marinus Johannes WMJ
TITLE OF INVENTION: Diagnostic reagents for the
TITLE OF INVENTION: detection of antibodies to EBV.
                                                         NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                        APPLICANT: Middeldorp, Jaap Michiel JM APPLICANT: van Grunsven, Wouterus Marin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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FILING DATE: 13-MAR-1992
ATTORNAL Y AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                            STREET:
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                                                                                                                                                                                                                                                                                                                                          Local
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9; Conserv
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AMINO ACID
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                         1330 Piccard Drive
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1330-A Piccard Drive
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MBER: 32,196
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                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                             FILING DATE: 03-APR-PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                           FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION UNMBER: EP 93202659.4
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MEDIUM TYPE: Floppy disk
                                                                     STRANDEDNESS:
                                                                                                                                                           NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/415,838
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Akzo-No. 6008327el Patent Department STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville
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TYPE: amino acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
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9; Conservative
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VENTION: Peptides and nucleic acid sequences

VENTION: related to the Epstein-Barr virus.
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Epstein-Barr virus
                                                    bs: single
linear
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Pred. No.
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US-09-354-231B-29
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Patent No. 6365717
GENERAL INFORMATION:
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LENGTH: 30
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/354,231B
CURRENT FILING DATE: 199-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF FILE REFERENCE: 07148-063002
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                   INFORMATION FOR SEQ ID NO: 6:
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es 9; Conser
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                     CURRENT APPLICATION DATA: application number: US/09/205,169
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Middeldorp, Jaap Michiel.
TITLE OF INVENTION: Peptides and nucleic acid sequences related to the Epstein-Barr virus.
                                                         ATTORNEY/AGENT INFORMATION: NAME: Gormley, Mary E.
                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 IAQKSEPHSLSSEALMRRAVSLVT 27
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                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                             APPLICATION NUMBER: 08/415,838 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAHECGHHAFSDYSLLDDVVGLVLHSS 30
                               NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409
                                                                                                                                                       FILING DATE: 04-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 Piccard Drive,
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Akzo-No.
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                                                                                                                                                                                                                                                                                                                                                                                       6365717el Patent Department
d Drive, Suite 206
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Pred. No. 86;
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ORGANISM: Epstein-Barr virus ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-205-169-6
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US-08-997-080-102
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; LENGTH: 30
; TYPE: PRT
; ORGANISM: Zear
                                                                                                                                                                                                                                                                                      Patent No.
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Matches
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APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND O:
TITLE OF INVENTION: FATTY ACID CONTENT
FILE REFERENCE: 07148-072001
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
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CURRENT APPLICATION NUMBER: US/No // FILING DATE:
                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                APPLICANT: WATS APPLICANT: TAN,
                                                                                                                                                           STREET: 2601 E
                                                                                                                                                     STATE:
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9; Conserv
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                                                                                                                                                                             2601 Elliott Avenue, Suite 4185
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Pred. No.
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Pred. No. 86;
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CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER:

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Best Local
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NAME: Sleath, Janet 37,007

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11001

TELECOMMUNICATION INFORMATION:

""" FDHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347 FILING DATE: August 29, 11996 ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11000.1002c2 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                  APPLICATION NUMBER: U FILING DATE: June 12,
                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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STRANDEDNESS: si
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2601 Elliott Avenue, Suite 4185
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Visser, Elizabeth
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2, 1997
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15 SEALMRRAVSLVTDS 29

Indels

0;

Gaps

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Matches

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US-08-873-970-102
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US-08-873-970-102
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              Query Match
Best Local :
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                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/7 FILING DATE: 29-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                MOLECULE TYPE: protein
                                                                                                                                                                                        TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                        TYPE: amino a
                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                 TOPOLOGY:
                                                                                                                                                                TELEX:
                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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nes 7; Conserv
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                                                                                                                       LENGTH:
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5. 6001361
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Similarity 7; Conserv
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                                                                                                      amino acid
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                                                                                                                      24 amino acids
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Visser, Elizabeth
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Scott, Linda
                                                                              ss: single
linear
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46.7%;
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            Score 32;
Pred. No.
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                         Length 24;
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RESULT 12
US-09-324-542-102
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         GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
                                                            Sequence 102, Application US/09324542 Patent No. 6328978
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                     Query Match
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PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tan, Fau.
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Brestidge, Ross
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/70:
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/87:
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 205-205-30563
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/095,855
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5. 6160093
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AEEKMEKAVSVARDS 23
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23-DEC-1997
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46.7%;
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Treatment and
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                                                                                                                                                                                                                      Indels
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                                                      RESULT 14
US-08-538-711A-16
         ; Sequence 16, Application US/08538711A ; Patent No. 5994062 ; GENERAL INFORMATION:
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APPLICANT:

MULSHINE, JAMES, L.

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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
US-09-205-426-102
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                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER APPLICATION NUMBER: 08/873,970
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER APPLICATION NUMBER: 08/705,347
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SEQ ID NO 102
LENGTH: 24
TYPE: PRT
ORGANISM: Mycobacterium vaccae
                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 102, Application Patent No. 6406704
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                      SEQ ID NO 102
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CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER FILING DATE: 1999-06-02

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                           ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                 TYPE: PRT
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NAME/KEY: UNSURE
LOCATION: (1)...(
                                                                                                                                                                                                                                                                   LENGTH: 24
                                                                                          Local
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                                   15 SEALMRRAVSLVTDS 29
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AEEKMEKAVSVARDS
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                                                                           Conservative
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                                                                                         22.7%;
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                                                                       Score 32; DB Pred. No. 94; 3; Mismatches
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                                                                                                            Length 24;
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                                                                       Gaps
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TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

AN EPITHELIAL PROTEIN AND DNA THEREOF FOR USE IN EARLY CANCER DETECTION

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08725027 Patent No. 6251586
             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,027
FILING DATE: 02-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: AN TITLE OF INVENTION: DN NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                APPLICANT: MULSHINE, JAMES, L.
APPLICANT: TOCKMAN, MELVYN, S.
TITLE OF INVENTION: AN EBITHELIAL PROTEIN AND
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
NUMBER OF SEQUENCES: 23
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/538,711A FILING DATE: 02-OCT-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                                                                                                                                                                            STREET: 345 PARK
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
STRANDEDNESS: Uni
TOPOLOGY: Linear
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                                                                                                                                                                COUNTRY: UZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
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                                   US/08/725,027
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Pred. No. 2.1e+02;
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; LENGTH: 29
; TYPE: Amino Acid
; STRANDEDNESS: Unkn
; TOPOLOGY: Linear
; MOLECULE TYPE: pepti
US-08-725-027-16
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Search completed: October Job time: 17 secs
                                                                                                              Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                            NAME: KATHRYN M. BROWN
REGISTION NUMBER: 34,556
REFERENCE, DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                              2 VPIAQKSEPHSLSSEAL-MRRAVS 24
                                                         6 VDAAMNARPHKVDGRVVEPKRAVS 29
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                                                                                                                                                                                                                                    Unknown
              2, 2003, 09:43:45
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                                                                                                                         4;
                                                                                                                                        Score 30.5; DB 3; Pred. No. 2.1e+02;
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                                                                                                                         Mismatches
                                                                                                                                                         DB 3;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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34.8
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB_PEP:*

/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB_PEP:*

/cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB_PEP:*

/cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*

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/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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//Ggn2_6/ptodata/2/pubpaa//US06_PUBCOMB.pep:*
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4 US-10-068-569-8
5 US-10-197-634-8
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0 US-09-798-116-22
0 US-09-965-967-25
0 US-09-965-967-25
0 US-09-964-761-47499
2 US-10-269-864-761-40008
0 US-09-864-761-40008
0 US-09-965-967-8
0 US-09-864-761-40008
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0 US-09-965-967-8
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Sequence 25, Appl
Sequence 25, Appl
Sequence 47499, A
Sequence 80, Appl
Sequence 40008, A
Sequence 6, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 24, Appli
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Sequence
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22, Appl
18, Appl
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8, Appli
8, Appli
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226-007-	26-007	10-226-007	174-41(-09-864-761-	864-761	-761-4394	8-424-5	-899-4	US-09-864-761-40837	US-09-864-761-42933	09-864-761-4171	864-761-	US-09-864-761-45203	US-09-965-738-279	64-761-	US-10-225-567A-1084	9-864-761-4	-10-051-643	-09-880-505-	-10-097-065	-567	9-864-7	-10-036-729	-771-904	US-09-995-297-29	-09-798-889-	-10-068-569-	-10-302-811-	US-10-293-371-45
1547,	153	1533,	e 272,	40411	42325		254,	e 59, Ap		42933,			45203, A	e 279,	Sequence 44657, A	e 1084,	40435,		102,	542,	Sequence 1480, Ap	3695	Sequence 6, Appli	e 29,	29, Ar	119, Ap	12,	5, A	Sequence 45, Appl

ALIGNMENTS

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Sequence 7, Application US/09939293

; Sequence 7, Application US/09939293

; Patent No. US20020132786A1

; GENERAL INFORMATION: ABOUT A PROPERTION OF POLYDEPTIDE OF INVENTION: AN IAP PEPTIDE OF POLYDEPTIDE OF INVENTION: AND METHODS OF USING THE SAME FILE REFERENCE: 480140.465

; CURRENT APPLICATION NUMBER: US/09/939,293

; CURRENT FILING DATE: 2001-08-24

; NUMBER OF SEQ ID NOS: 18

; SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Homo sapiens US-09-939-293-7
                                                                                                                                                           RESULT 2
US-10-068-569-8
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US-09-939-293-7
Sequence 8, Application US/10068569
Publication No. US20020160975A1
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alpemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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Pred. No. 8.5e-15;
Mismatches 0;
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; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: M is methionine sulfoxide
US-09-798-116-20
                                                                                                                                                                                      APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
TITLE OF INVENTION: NO. US20020110851A1el Po
FILE REFERENCE: 10338-004US
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
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US-10-197-634-8
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                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09798116 Patent No. US20020110851A1 GENERAL INFORMATION:
                                                                                                                                        NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ALDEMTI, Emad S.
TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
TITLE OF INVENTION: IAP-CASPASE INVERACTION
FILE REFERENCE: 480140.479
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/197,634
CURRENT FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity 93.3
Matches 14; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 15
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10197634 Publication No. US20030073629A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
                                                                               LENGTH: 13
TYPE: PRT
ORGANISM: synthetic
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                    FEATURE:
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93.3%;
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93.3%;
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Pred. No. 0.00034;
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0.00034;
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                                QΥ
                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-18
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US-09-965-967-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: synthetic US-09-798-116-22
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US-09-798-116-22
; Sequence 22, Application U
; Patent No. US20020110851A1
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                                                                                                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 18 LENGTH: 10
                                                                   Matches
                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Shi, Yig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 22 LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09965967 Patent No. US20020177557A1
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
                                                                                                                                                                                                                                                                           APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
FILE REFERENCE: PU-0031 (01-1739-1)
FILE REFERENCE: PU-0031 (01-1739-1)
CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,574
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vaux, David
TITLE OF INVENTION: No. US20020110851A1el Polypeptides, Modulatory Agents Therefor FILE REFERENCE: 10338-00405
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 30
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                                                               Local Similarity
tes 10; Conserv
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                               1 AVPIAQKSEP 10
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AVPIAQKSEP
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ilarity 100.0%;
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100.0%; Pr
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100.0%;
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Pred. No. 0.37;
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                                                               Mismatches
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0.0034;
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RESULT

US-09-965-967-25

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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: synthetic US-09-798-116-25
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SEQ ID NO 25
LENGTH: 13
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SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 29
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                 Sequence 47499, Application US/09864761 Patent No. US20020048763A1
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions and Methods For Regulating Apoptosis
FILE REFERENCE: PU-0031 (01-1739-1)
CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
TITLE OF INVENTION: No. US20020110851Alel Polypeptides, Modulatory Agents Therefor an
FILE REFERENCE: 10338-004US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/256,830 PRIOR FILING DATE: 2000-12-20
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100.0%; Pred. No.
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Pred. No.
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31;
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US-10-269-806-80
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APPLICANT: Min, Hosung
APPLICANT: Sitney, Karen
APPLICANT: Sitney, Karen
APPLICANT: Hartley, Cynthia
TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic Activity
FILE REFERENCE: A-750
CURRENT APPLICATION NUMBER: US/10/269,806
CURRENT FILING DATE: 2002-10-10
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin version 3.1
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO AC022267.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER,
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
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FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
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Pred. No. 76;
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LENGTH: 25
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                                                                               NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                           PRIOR FILING DATE:
                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/774,203
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                      LENGTH: 29
TYPE: PRT
ORGANISM: Homo sapiens
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                                                               ID NO 40008
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                                                                                                                                                                  APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-27
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Chen, Wensheng
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NUMBER: US 09/632,366
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Pred. No.
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                                                                                 Engine vers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
2.2e+02;
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; ORGANISM: H
US-09-965-967-8
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US-09-965-967-8
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US-09-939-293-6
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                                                                                        SOFTWARE: Pa
SOFTWARE: Pa
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 7

TYPE: PRT

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Shi, Yig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE TITLE OF INVENTION: AND METHODS OF USING THE SAME FILE REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEC.
Query Match
                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09965967 Patent No. US20020177557A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 7; Conserv
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Best Local
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PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/256,830
PRIOR FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                    APPLICANT: Shi, Yigong
TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
FILE REFERENCE: PU-0031 (01-1739-1)
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/965,967
CURRENT FILING DATE: 2001-09-28
                                                                                                                                               NUMBER OF SEQ ID NOS: 30
                                                                       TYPE: PRT
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R INFORMATION:
R INFORMATION:
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                                                                                                                            PatentIn version 3.1
                                                        Homo
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                                                      sapiens
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NN: EXPRESSED IN LING, SIGNAL = 8

NN: EXPRESSED IN PLACENTA, SIGNAL = 7.2

NN: EXPRESSED IN HEART, SIGNAL = 7.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 7.8

NN: EXPRESSED IN BARIN, SIGNAL = 7.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 7.5

NN: EXPRESSED IN HELA, SIGNAL = 8.2

NN: EXPRESSED IN HELA, SIGNAL = 8.2

NN: EXPRESSED IN HELA, SIGNAL = 8.6

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6
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 23.4%;
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 Score 33;
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Pred. No. 3.1e+02;
2; Mismatches 7;
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 DB
 10;
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 Length 7;
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CURRENT APPLICATION UMBER: US/10/293,371
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,934
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/332,300
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEO ID NOS: 85
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
7; Conserve
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; OTHER INFORMATION: Synthetic
US-10-293-371-1
; ORGANISM: Artificial Sequence; FEATURE:
; OTHER IMFORMATION: Synthetic US-10-293-371-24
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                                                                                                              NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/10293371 Publication No. US20030157522A1
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/293,371 CURRENT FILING DATE: 2003-04-08 PRIOR APPLICATION NUMBER: US 60/370,934 PRIOR FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US 60/332,300 PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LISTON, PETER
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
TITLE OF INVENTION: Interaction Screens
FILE REFERENCE: 07891/030002
                                                                                                                                                                                                                                                                                       APPLICANT: BOUDREAULT, ALAIN
APPLICANT: KORNELUK, ROBERT G.
APPLICANT: LACASSE, ERIC
APPLICANT: LACASSE, ERIC
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
TITLE OF INVENTION: Interaction Screens
FILE REFERENCE: 07891/030002
                                                                              TYPE: PRT
                                                                                                  ENGTH:
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Pred. No. 5.2e+05;
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Query Match 23.4%; Score 33; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 AVPIAQK 7
| 1||||| Db 1 AVPIAQK 7
| Search completed: October 2, 2003, 09:44:16

Job time: 23 secs
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Oldso MAN TE JEWO SIHIL

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RESULT 13
US-09-798-116-6
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US-09-798-116-9
                                                                                 SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 177
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09798116 Patent No. US20020110851A1 GENERAL INFORMATION:
   Best Local
Matches 2
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Best Local Similarity
Matches 23; Conserv
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                                    Query Match
                                                                                                                                                                   TITLE OF INVENTION: No. US20020110851Alel Polypeptides, Modulatory Agents Therefor at FILE REFERENCE: 10338-004US CURRENT APPLICATION NUMBER: US/09/798,116 CURRENT FILING DATE: 2001-03-02 PRIOR APPLICATION NUMBER: AU PQ5995/00 PRIOR FILING DATE: 2000-03-02 NUMBER: OF SEQ ID NOS: 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
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APPLICANT: Vaux, David
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
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 . Similarity 95. 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.6%; Score 108; DB 10; llarity 100.0%; Pred. No. 8.5e-09; Conservative 0; Mismatches 0;
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                  74.58;
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90.0%;
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Pred. No. 8.4e-12;
Pred. No. 8.4e-12;
Score 105; DB 10;
Pred. No. 2.5e-08;
1; Mismatches 0;
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Best Local Similarity
Thes 14; Conserve
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; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-8
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Search completed: October Job time: 24 secs
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US-10-068-569-8
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Best Local Similarity
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APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
FILE REFERENCE: 480140.475
                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 480140.479
CURRENT APPLICATION NUMBER: US/10/197,634
CURRENT FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
TITLE OF INVENTION: IAP-CASPASE INTERACTION
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CURRENT FILING DATE: 2002-02-06
NUMBER OF SEO ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alnemri,
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TYPE: PRT
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93.3%;
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Pred. No. 0.00
1; Mismatches
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RESULT 9
US-09-798-116-2
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Sequence 2, Application US/09798116
                                                                                                                                                                                                                                                                                                          SEQ ID NO 348
LENGTH: 239
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Best Local
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PRIOR EILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 60/356,934
PRIOR EILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US 09/388,221
PRIOR FILING DATE: 1999-09-01
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PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
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APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
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APPLICANT: MATSU
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CURRENT APPLICATION NUMBER: US/10/141,618
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
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Pred. No. 9.8e-14;
; Mismatches 0;
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Pred. No. 9.8e-14;
Mismatches 0;
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RESULT 11
US-09-798-116-9
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                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Verhagen, Anne Marie
APPLICANT: Ekert, Paul
APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
TITLE OF INVENTION: No. US20020110851a1el Polypeptides, Modulatory Agents Therefor
FILE REFERENCE: 10338-004US
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
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APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
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CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PQ5995/00
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: AU PQ5995/00 PRIOR FILING DATE: 2000-03-02 NUMBER OF SEQ ID NOS: 25
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TYPE: PRT
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29; Conserv
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Vaux, David
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96.78;
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Pred. No. 2.8e-13;
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Pred. No. 2.8e-13;
1; Mismatches 0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-11
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NUMBER OF SEQ ID NO:
SOFTWARE: FASTSEQ f
SEQ ID NO 11
TENGTH: 35
                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Allemri, Emad S.
TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: 480140.465
FULL REFERENCE: 480140.465
CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09939293
Patent No. US20020132786A1
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Matches
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Best Local
                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
                                                               Matches
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CURRENT APPLICATION NUMBER: US/09/939,293
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAMI
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                        LENGTH: 40
TYPE: PRT
                                                                           Local
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ilarity 100.0%;
Conservative 0
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                                                       Score 141; DB 10;
Pred. No. 1.2e-14;
; Mismatches 0;
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Pred. No. 1.2e-14;
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Pred. No. 1e-14;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-116-7
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                                                                             Best Local Similarity Matches 30; Conserv
                                                                                                                   Query Match
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LENGTH: 227
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Best Local Similarity
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Patent No. US20020110851A1
                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989 -
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NO. US20020110851A1el Polypeptides, Modulatory Agents Therefor E1LE REFERENCE: 10348-004US
CURRENT APPLICATION NUMBER: US/09/798,116
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: AU PO5995/00
PRIOR APPLICATION NUMBER: AU PO5995/00

PRIOR APPLICATION NUMBER: AU PO5995/00

PRIOR APPLICATION NUMBER: AU PO5995/00
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APPLICANT: Ekert, Paul
APPLICANT: Vaux, David
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
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NUMBER OF SEQ ID NOS: Z5
                                                                                                                                                                             NAME/KEY: SITE LOCATION: (1)
OTHER INFORMATION:
                                                                                                                                                                                                                                          ORGANISM: HOMO FEATURE:
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                  1 AVPIAQKSEPHSLSSEALMRRAVSLVTDST 30
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Pred. No. 9.2e-14;
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RESULT 7 US-10-141-618-14

Sequence 14, Application US/10141618 Publication No. US20030165887A1 GENERAL INFORMATION:

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Result
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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    /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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10 US-09-939-293-9
10 US-09-925-297-591
12 US-10-141-618-14
15 US-10-153-668-348
16 US-09-798-116-9
17 US-09-798-116-9
18 US-09-798-116-8
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11 US-10-068-569-8
15 US-10-197-634-8
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Sequence 7, Appli
Sequence 11, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 591, App
Sequence 14, Appli
Sequence 348, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 8, Appli
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US-09-39-293-7
Sequence 7, Application US/09939293
; Patent No. US20020132786A1
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APPLICANT: Alnemat, Emad S.
APPLICANT: Alnemat, Emad S.
TITLE OF INVENTION: AN IAP PEPTIDE OF POLYPEPTIDE
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: 480140.465
                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 7
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT FILLING DATE: 2001-08-24
NUMBER OF SEO ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 30
TYPE: PRT
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us-09-764-877-1372	-761-	À			US-10-137-418A-3	US-10-106-698-4636	US-10-067-741-7	US-09-560-150-7	US-09-372-044-2	US-08-870-434-7	US-08-825-486-2	US-10-021-425-27		US-09-925-301-867	-299	09-925-299-	-09-890-688-	-10-078-090	US-10-001-857-201	US-09-801-368-152	US-09-815-242-11036	US-10-193-692-2	US-10-193-692-4	US-10-156-761-7801	-09-965-967-	5-967-	-09-798-116-1	US-09-798-116-22	us-09-798-116-20
Sequence 1372, Ap	Sequence 8391, Ap	Sequence 2, Appli	Sequence 8, Appli	79	3, App	46	7,	7,	Sequence 2, Appli	7,	2, Ap	27,	e 24,	367, Ap	Sequence 1546, Ap	1546,	110,	188,	e 201,	(U	1103	2,	4, App	780	e 25,	e 18,	e 10,	Sequence 22, Appl	Sequence 20, Appl

ALIGNMENTS

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RESULT 2
US-09-939-293-11
; Sequence 11, Application US/09939293
; Patent No. US20020132786A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; FILE REFERENCE: 480140.465
; CURRENT APPLICATION NUMBER: US/09/939,293
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-939-293-7
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Similarity 100.0%;
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RESULT 8
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                                                                                                                                                                                                                                                                    Fluorosceinated
                                                                                                                                                                                                                                                                                                         09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                       ABB76228 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                         WO200230959-A2
                                                                                                                                            Synthetic.
                                                                                                                                                                                                       human;
                                                                                                                                                                                                                                                                                                                                                 ABB76228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-2000; 2000US-0687549
                                                                               Modified-site
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a peptide derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fesik SW, Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200230959-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                            smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                   inhibitor of apoptosis protein; IAP; apoptosis;
; cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                                  smac
                                                                                                  Location/Qualifiers
                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26pp;
                                                                                                                                                                                                                                                               (DIABLO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                            "N-terminal fluorescein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "optional C-terminal protecting group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Betz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP,
                                                                                                                                                                                                                                                               derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from human second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
ABG72319
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Best Local
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WPI; 2003-074681/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                     Verhagen AM,
                                                                                                                                                                                                     15-AUG-2002.
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG72319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                             HALL
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fluorescence polarisation-based competition assay designed to determine the binding affinity of variant smac peptides (see ABB76206-27) to the Bir-3 and Bir-2 domains of XIAP, an inhibitor of apoptosis protein (IAP) family member. Claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                             inhibitor of apoptosis; IAP; cancer; vascular disease; hepati autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence corresponds to amino acids 1-9 of human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of depotosis binding protein with low pI (DIABLO), but is fluorosceinated. The peptide was used in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000; 2000AU-0005995
                                                                                                                                            02-MAR-2001; 2001US-0798116
                                                                                                                                                                                                                                            US2002110851-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       Human; pro-apoptotic
inhibitor of apoptosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG72319 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 14; 26pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-2000; 2000US-0687549
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                                                                                                                                                                                                                                                                                                                                      liver disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-444169/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pro-apoptotic protein DIABLO peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVPIAQKSE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                               INST MEDICAL RES WALTER &
Ekert PG,
                                                                                                                                                                                                                                                                                                                                        immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; DIABLO; cell death; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Betz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                                                                                                                                                                                            hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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^(ntq2) YNA 18 30A9 21HT

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RESULT 10
ABG24798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC designated DIABLO, or its biologically active fragment of 8 amino acids (c) in length. Also included are the polyncheotide encoding DIABLO, (c) expression vectors, transformed host cells, producing a biologically contacting an inhibitor of apoptosis (IAP) (c) active fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP) (c) with a fragment of the polypeptide, and detecting a reduction in activity of with cell death activity or which reduces IAP activity, an antigentic detecting producing a natural or synthetic variant of DIABLO (c) with cell death activity or which reduces IAP activity, an antigentic detecting brablo in a biological sample (by contacting the sample composition for the presence of an IAP/DIABLO or its fragment, commodulating the death of a cell (by contacting a cell with an activity of a composition for treatment/prophylaxis of a DIABLO related committees the level and/or functional activity of a condition comprising an agent which modulates cell death. An composition for an agent which modulates cell death. An comprising mature or pro-human DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO polypeptide, is condition activation of DIABLO, such as cancer, vascular construction activation of DIABLO, such as cancer, vascular construction activation of DIABLO, such as cancer, vascular construction activation activation of DIABLO, such as cancer, vascular construction activation activation of DIABLO, such as cancer, vascular construction activation activation of DIABLO, such as cancer, vascular construction activation activation associated with heart construction activation activation associated with heart construction activation activation activation associated with heart construction activation activation associated with heart construction activation activati
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Best Local Similarity
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               31-MAR-2000;
23-AUG-2000;
                                                                            30-MAR-2001; 2001WO-US08631.
                                                                                                                     11-OCT-2001
                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #24789
                                                                                                                                                                                                                                                                                                                                                                                                ABG24798;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG24798 standard; Protein; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated designated DIABLO, or its biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell death or apoptosis e.g. cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 AVSLVTDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AVSLVTDST 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
               2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in isolated pro-apoptotic polypeptide,
biologically active fragment of 8 am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score 40; DB; Pred. No. 21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 11
ABB76218
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                   Modified-site
                                                                                                                                     Misc-difference
                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                        Homo sapiens:
                                                                                                                                                                                                                                                        DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                            Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                  ABB76218;
                                                                                                                                                                                                                                                                                                                                                                                                   ABB76218 standard;
                                                  WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags polymucleotides are also used in diagnostics, as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                           human; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 55157; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying expressed genes. (I) is useful in gene therapy techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VPIAQKSEPHSLSSEALMRRAVS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS88985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPVHQQMRMHNVAGRATVRQQIS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                         cytostatic; mutant; mutein
                                                                                                                                       Location/Qualifiers
                                                                                   /note=
                                                                                                                   /note= "wild-type Ala substituted by Phe"
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.7%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                               "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
32;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method involves detecting the presence of large and small caspase subunits after contacting cell transformed with the vector expressing (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of caspase-3, caspase-3 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the N-terminal amino acid sequence of Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    death pathway; and (c) measuring the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase, where the inhibitor inhibits activation or activity of caspase-3, caspase-7 or caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-mediated apoptosis which involves contacting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or candidate enhancer; and detecting cell viability, where an increase in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:
(a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, replacing the mitochondrial targeting sequence (residues 1-55 of (I)), and an residues 56.00 of (I)) and an inhibitor of BID (Boll) interacting domain) with a compound to be tested for apoptotic inhibiting activity, (b) incubating the cell populations with a direct stimulus of the cell
                                                            Rat; pro-apoptotic protein; DIABLO; cell death; apoptosis;
Inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic disease;
autoimmune disease; neurodegenerative disease; tissue damage;
muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Smac peptides and polynucleotides for stimulating apoptosis in neoplastic overexpresses inhibitor of caspase, and
  Rattus
                                                                                                                                                                         Rat partial sequence
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                                                                                                                                                                                                                   29-JAN-2003
                                                                                                                                                                                                                                                                                                      ABG72303 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulating
                                                                                                                                                                                                                                                              ABG72303
                                            liver
                                            disease;
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7; Conser
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                                                                                                                                                                     pro-apoptotic protein DIABLO
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
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with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO relate condition comprising an agent which reduces the level/activity of a polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity cappitide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autoimmune disease and neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                designated DIABLO, or its biologically active fragment of 8 amino aci in length. Also included are the polyucclectide encoding DIABLO, expression vectors, transformed host cells, producing a biologically active fragment of DIABLO (by contacting an inhibitor of apoptosis (I with a fragment of the polypeptide, and detecting a reduction in acti of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample detecting DIABLO) in a biological sample (by contacting the sample)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell death or apoptosis \mathbf{e}_i g . cancer \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002110851-A1
                                                                                          attack, or hepatic tissue damage associated with a liver disease DIABLO is also useful for treatment and/or prophylaxis of conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000; 2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2001; 2001US-0798116
                                                                    associated with cell death or apoptosis. The
                                                                                                                                         disease, tissue damage or muscular tissue damage associated with heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 35; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verhagen AM,
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                                              partial rat DIABLO
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                                                                         present sequence
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            1 AVPIAQK 7
                          7; Conserv
                           Conservative
                                 100
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                                 Score 33; [
Pred. No. 2.
                           Mismatches
                                  DB 24; Length 84;
2.9;
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RESULT 15 ABG72302

ABG72302 standard; Protein;

ABG72302;

29-JAN-2003 (first entry)

Human partial sequence for pro-apoptotic protein DIABLO

autoimmune disease; Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepat neurodegenerative disease; tissue damage; hepatic disease;

(OTARU) XNALE BLANK (USPTO)

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Database
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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49.6
44.7
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ABB76208
ABB71314
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                                             Human Smac protein
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Human smac (DIABLO
Human smac (DIABLO
                                                                                                                                                                                                                                                            Description
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                                                                                                                                                                              Inhibitor of apopt
Human smac (DIABLO
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Peptide #3805 enco	629	22	20	22.7		u
Human smac (DIABLO	ABB76219	23	9	22.7	32	4
	AAY95833	21	27	23.0		ω
Epstein-Barr	AAW99319	20	30	23.4		N
Epstein-Barr vi	AAR74988	16:	30	23.4		_
	AAR42319	14	30	23.4		0
Human immune/ha	AAM83269	22	26	23.4		9
Human secr	AAY45327	20	24	23.4		8
Smac-7 AV pep	AAU78487	23	7	23.4		7
Inhibitor o	AAU78434	23	7	23.4		σ
Human smac (D	ABB76213	23	7	23.4	33	5
Human MAGE-3 s	AAU85044	23	30	23.8	ω.	4
Human peptide	ABG43702	23	29	•	ω.	ω
Peptid	AAM33999	22	29	23.8	ω.	N
Peptide #6543 enco	AAM20109	22	29	•	w	_
Human bone marrow	AAM73813	22	29	•	ω.	0
ain ex	AAM61105	22	29	•	ω.	9
ein #6709	ABB24710	22	29	•	ω.	80
Peptide #781	ABB40307	22	29	23.8		7
Human liver p	ABG55563	22	29	•	ω.	0
BRCA2 cancer	AAW25067	18	26	•		G
Human	ABB76223	23	9	•		4
Human smac (ABB76216	23	9	•		ω
Human smac	ABB76211	23	9	•		N
Huma	ABB76210	23	9	•		_
Peptide #117	ABB44274	22	25	•		0
liver	964	22	25	•		9
smac (622	23	9	•		æ
smac (o	23	8	•		7
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smac (62	23	9	27.0		_
Novel human diagno	ABG24798	22	30	27.7		0

ALIGNMENTS

RESULT 1 AAU78435

AAU78435 standard; Peptide; 30

AAU78435;

18-JUN-2002 (first entry)

Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N30.

Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; mutant; tumour.

Homo sapiens

Synthetic.

28-FEB-2002.

WO200216418-A2

24-AUG-2001; 2001WO-US26492

24-AUG-2000; 2000US-227735P.

(UYJE-) UNIV JEFFERSON THOMAS

WPI; 2002-304115/34

Novel Smac peptides and polynucleotides encoding the peptides, useful

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RESULT 2
ABB76208
ID ABB7
XX ABB7
AC ABB7
XX U9-A
XX U1AB7
DT U9-A
XX DIAB
DE Huma
XX DIAB
KW DIAB
KW huma
XX HOMC
XX HOMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated Smac peptide or polypeptide (I) cand an isolated nucleic acid (II) encoding (I). Also described is a CC method of identifying a compound that inhibits apoptosis, comprising: (a) separately contacting several cell populations expressing a CC cytosolic Smac (a Smac isoform that begins with MKSDFYF sequence, CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)), CC and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting CC domain) with a compound to be tested for apoptotic inhibiting activity; (b) incubating the cell populations with a direct stimulus of the cell cell populations, where inhibition of the specific apoptotic activity is cell populations, where inhibition of the specific apoptotic activity is cell populations, where inhibition of the specific apoptotic activity is cell populations, where inhibition of the specific apoptotic activity is cell population, where inhibition of the specific apoptotic activity is cell population, where inhibitor of apoptosis, (I) and (II) cell population of inhibitor of apoptosis, (I) and (II) cell population or activity of caspase-3, caspase-7 or ceapase-9. Perferably the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-7 cell transformed or transferted with a vector expressing (I) with a candidate inhibitor or call viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the cell presence of an enhancer optionally, the cell presence of an inhibitor or expressing indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an inhibitor or expressing indicates the presence of an enhancer. Optionally, the cell presence of an enhancer optionally, the cell presence of an inhibitor of and indicates the presence of an enhancer. Optionally, the cell presence of an en
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                                                                            Modified-site
                                                                                                                                         Homo
                                                                                                                                                                             human;
                                                                                                                                                                                                                                    Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                            09-AUG-2002
                                                                                                                                                                                                                                                                                                                  ABB76208;
                                                                                                                                                                                                                                                                                                                                                   ABB76208 standard; Peptide;
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30; Conser
                                                                                                                                                                                               smac;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                           inhibitor of apoptosis protein;
cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA;
                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                      "optional C-terminal protecting group
                                                                                                                                                                                                                                peptide.
                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 141; DB 23;
Pred. No. 2.2e-16;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                         IAP; apoptosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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13-JUL-2001; 14-DEC-2001; 15-JUL-2002; 23-JAN-2003

2001US-305378P 2001US-340163P 2002WO-US22658

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RESULT 3
ABP71314
Вb
                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uM, respectively, for the present peptide, compared with 0.42 +/-
0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac.
Modification of the N-terminal alanine destroys binding affinity to
XTAP. For example, N-terminal alanine with glycine, propionic acid
or isobityric acid all resulted in Kd values for Bir-3 and for Bir-2
of over 1,000 uM. The claimed peptides can be used to identify
candidate substances which induce or promote apoptosis in cells.
The assay involves determination of the ability of candidate
compounds to disrupt the binding interaction between a smac (DIABLO)
                                                                                                                                                                               Omi; HtrA2; serine protease; inhibitor of apoptosis protein; IAP; caspase; apoptosis; cytostatic; immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                                         ABP71314 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a peptide derived from wild-type human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived peptides (see ABB/6208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. K values for Bir-3 and Bir-2 are 0.69 +/- 0.05 uM and 6.7 +/- 0.7
                                                                                                             WO2003006680-A2
                                                                                                                                       Homo sapiens
                                                                                                                                                                   vasotropic;
                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                      28-APR-2003
                                                                                                                                                                                                                                                                                 ABP71314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide and an IAP family member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2002
                                                                                                                                                                                                                         Smac
                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                              AVPIAQKSEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                              AVPIAQKSEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 7; 26pp;
                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to kill cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                         N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Betz
                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells
                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bir-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0,

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RESULT 4
ABG772314
ID ABG7
XX
AC ABG7
XX
AC ABG7
XX
DT 29-
DT 29-
XX
KW Hun
KW Hun
KW Hun
KW Bu'
KW Bu'
KW Hun
KW 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides encoding an Omi (Serine protease) peptide or polypeptide. The Omi peptide specifically binds to portion of an Inhibitor of Apoptosis Protein (IAP). The Omi polypeptide induces caspase-independent apoptosis, or fails to have serine protease activity. The Omi peptides are useful for regulating or altering apoptosis, specifically caspase-mediated apoptosis, and as immunogens for raising antibodies. Enhancers of apoptosis are useful for treating cancers, tumours or for destroying cells that mediate autoimmune diseases. Compositions may also be used for the treatment of diseases associated with inappropriate activation of apoptosis such as neurodegenerative diseases and ischaemic injury. The antibodies can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic disease; autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative diseases and ischaemic injury. The antibodies can be used in isolating Omi peptides, polypeptides and their variants, in identifying molecules that interact with Omi peptides and polypeptides, and in inhibiting or enhancing the biological activity of Omi peptides and polypeptides. Sequences ABF71310-315 represent fragments of various the biological activity of the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Omi nucleic acids and peptides that bind to an inhibitor of apoptosis proteins, useful for regulating or altering caspase-me apoptosis and for treating cancer, tumor, or autoimmune diseases
                                                                                                                                                   02-MAR-2001; 2001US-0798116
                                                                                                                                                                                                                                                                                US2002110851-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG72314 standard; Peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                (HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                                            02-MAR-2000; 2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAP-binding proteins, used to determine Omi as a IAP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pro-apoptotic protein DIABLO peptide sequence #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVPIAQKSEPHSLSS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPIAQKSEPHSLSN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; 83pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogen
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.68;
                                                                                                                                                                                                                                                                                                                                   "Methione is methionine sulphoxide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; I
7.7e-05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to an inhibitor of altering caspase-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 5
ABG72316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC with an IAP and detecting the presence of an IAP/DIABLO complex),

CC modulating the death of a cell (by contacting a cell with an

CC agent, which modulates the level and/or functional activity of a

CC polypeptide, a composition for treatment/prophylaxis of a DIABLO related

CC polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is

CC useful for screening for an agent which modulates cell death. An

CC antigen-binding molecule is useful for detecting DIABLO in a biological

CC sample. The agent which modulates the level and/or functional activity of

CC a polypeptide comprising mature or pro-human DIABLO polypeptide, is

CC useful for the treatment and/or prophylaxis of a condition associated

CC useful for the treatment and/or prophylaxis of a condition associated

CC with expression or activation of DIABLO, such as cancer, vascular

CC disease, hepatic disease, autoimmune disease and neurodegenerative

CC disease, tissue damage or muscular tissue damage associated with heart

CC attack, or hepatic tissue damage associated and aliver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence represents a partial peptide sequence from human DIABLO, identified by protein sequencing of a protein (later identified as DIABLO) which co-precipitates with the human IAP protein MIHA (not defined).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length. Also included are the polynucleotide encoding DIABIO, expression vectors, transformed host cells, producing a biologically active fragment of DIABIO (by contacting an inhibitor of apoptosis () with a fragment of the polypeptide, and detecting a reduction in action of the IAP), producing a natural or synthetic variant of DIABIO with cell death activity an antigenbinding molecule that specifically binds to DIABIO or its fragment, detecting DIABIO in a biological sample (by contacting the sample of the producing bills).
                                                                                                                                       Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepati autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                     ABG72316 standard; Peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell
                                                                                                                                                                                                                                                                                     29-JAN-2003
                                                                                                                                                                                                                                                                                                                              ABG72316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   designated
in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 4; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       death or apoptosis e.g. cancer
                                                                             Homo sapiens
                                                                                                                      liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Verhagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-074681/07
                                                                                                                      disease;
                                                                                                                                                                                                                                            pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEPHSLSSEALMR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ekert PG,
                                                                                                                    immunogen
                                                                                                                                                                                                                                            protein DIABLO peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaux DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24;
0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13
                                                                                                                                                                                                                                              #12.
                                                                                                                                                                                  hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IAP)
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0;

US2002110851-A1

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RESULT 6
ABB76209
ID ABB7
XX ABB7
XX ABB7
AC ABB7
XX O9-A
XX U9-A
XX U1AB
CX Huma
XX DIAB
XX DIAB
XX Homa
XX Homa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC in length. Also included are the polynuclectide encoding DIABLO.

CC expression vectors, transformed host cells, producing a biologically

CC expression vectors, transformed host cells, producing a biologically

CC with a fragment of DIABLO (by contacting an inhibitor of apoptosis (IAP)

CC with a fragment of the polypeptide, and detecting a reduction in activity

CC with cell death activity or which reduces IAP activity, an antigen-

CC binding molecule that specifically binds to DIABLO or its fragment,

CC detecting DIABLO in a biological sample (by contacting the sample

CC with an IAP and detecting the presence of an IAP/DIABLO complex),

CC modulating the death of a cell (by contacting a cell with an

CC agent, which modulates the level and/or functional activity of a

CC polypeptide), a composition for treatment/prophylaxis of a DIABLO is

CC condition comprising an agent which reduces the level/activity of a

CC polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is

CC useful for screening for an agent which modulates cell death. An

CC useful for screening for an agent which modulates cell death. An

CC apolypeptide comprising mature or pro-human DIABLO in a biological

CC sample. The agent which modulates the level and/or functional activity of

CC useful for the treatment and/or prophylaxis of a condition associated

CC with expression or activation of DIABLO, such as cancer, vascular

CC disease, hepatic disease, autoimmune disease and neurodegenerative

CC attack. or hematic fissue damage associated with heart
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attack, or hepatic tissue damage associated with a liver disease. DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence represents a partial peptide sequence from human DIABLO, identified by protein sequencing of a protein (later identified as DIABLO) which co-precipitates with the human IAP protein MIHA (not defined).
Homo sapiens
                                                          DIABLO;
                                                                                                  Human smac (DIABLO) derived peptide
                                                                                                                                            09-AUG-2002
                                                                                                                                                                                      ABB76209
                                                                                                                                                                                                                        ABB76209 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated pro-apoptotic polypeptide, designated DIABLO, or its biologically active fragment of 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              death or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2000;
                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
13; Conser
                                                          smac;
                                                                                                                                                                                                                                                                                                                               SEPHSLSSEALMR 13
                                                                                                                                                                                                                                                                                                                                                                  SEPHSLSSEALMR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 4; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative (
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000AU-0005995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0798116
                                                    inhibitor of apoptosis protein; IAP; apoptosis;
                                         cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaux DL
                                                                                                                                                                                                                            و
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63;
Pred. No.
                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 7
ABB76229
ID ABB7
DЪ
                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                        second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI (DIABLO). The peptide is one of 12 claimed smac (DIABLO) the peptide is one of 12 claimed smac (DIABLO) the pi claimed smac (DIABLO). The peptide is one of 12 claimed smac (DIABLO) derived peptides (see ABP56208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Repetides for Bir-3 and Bir-2 are 0.43 +/- 0.6 uM and 6.0 +/- 0.9 uM, respectively, for the present peptide, compared with 0.42 +/- 0.0 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac. Modification of the N-terminal alanine destroys binding affinity to XIAP, and mutation of the valine, proline or isoleucine also causes some loss of binding. Amino acids C-terminal to the isoleucine are not important for binding. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac (DIABLO) peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                        Synthetic
                                                                                                                  DIABLO;
                                                                                                                                               Human smac (DIABLO) derived peptide.
                                                                                                                                                                             09-AUG-2002 (first entry)
              Misc-difference
                                                                       Homo sapiens
                                                                                                       human;
                                                                                                                                                                                                              ABB76229;
                                                                                                                                                                                                                                        ABB76229 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a peptide derived from wild-type human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fesik SW, Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001; 2001WO-US32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                     cancer;
                                                                                                                   smac;
                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                              AVPIAQKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 7; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                  inhibitor of
                                                                                                     cytostatic;
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                        29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Betz
                                                                                                     mutant; mutein.
                                                                                                                  apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP,
                                                                                                                                                                                                                                                                                                                                                                                          Score 42;
Pred. No.
                                                                                                                                                                                                                                          ΑA
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu 2,
                                                                                                                                                                                                                                                                                                                                                                                        DB 23; 1
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olejniczak ET,
                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/note= "N-terminal acetyl"

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RESULT 8
ABB76228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76209) acetylated. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 uM for the present peptide, compared with 0.43 +/ 0.06 uM and 6.0 +/ 0.9 uM, respectively, for the corresponding wild-type peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondria derived activator of caspase (smac), also known direct inhibitor of apoptosis binding protein with low pI (DIABLO), but with the native N-terminal alanine residue (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptide derived from wild-type activator of caspase protein useful f substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a peptide derived from human second mitochondria derived activator of caspase (smac), also known
                                                                                                                                    Synthetic
                                                                                                                                                                                    DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
human; cancer; cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                  Fluorosceinated
                                                                                                                                                                                                                                                                                     09-AUG-2002
                                                                                                                                                                                                                                                                                                                          ABB76228
                                                                                                                                                                                                                                                                                                                                                           ABB76228 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-444169/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-2000; 2000US-0687549
                         WO200230959-A2
                                                                               Modified-site
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001; 2001WO-US32121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200230959-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                  smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                            /note= "N-terminal fluorescein'
                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26pp; English
                                                                                                                                                                                                                                            (DIABLO) derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betz
                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SP,
                                                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human second mitochondria derived for identifying candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
RESULT 9
ABG72319
ID ABG7
XX ABG7
AC ABG7
XX ABG7
XX Huma
XX Huma
XX Huma
XX Inii
KW Autc
XX M Musc
XX Homc
XX Hom
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
 WPI; 2003-074681/07
                                                                         (HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG72319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                     liver
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fluorescence polarisation-based competition assay designed to determine the binding affinity of variant smac peptides (see ABB76206-27) to the Bir-3 and Bir-2 domains of XIAP, an inhibitor of apoptosis protein (IAP) family member. Claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                            Human; pro-apoptotic protein; DIABLO; cell death; apoptosis; inhibitor of apoptosis; IAP; cancer; vascular disease; hepatic autoimmune disease; neurodegenerative disease; tissue damage; muscular tissue damage; heart attack; hepatic tissue damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide derived from wild-type activator of caspase protein useful f substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG72319 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence corresponds to amino acids 1-9 of human second mitochondria derived activator of caspase (smac), also as direct inhibitor of apoptosis binding protein with low pI (DIABLO), but is fluorosceinated. The peptide was used in a
Verhagen AM,
                                                                                     02-MAR-2000;
                                                                                                                                02-MAR-2001; 2001US-0798116
                                                                                                                                                                                                                      US2002110851-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pro-apoptotic protein DIABLO peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-2000; 2000US-0687549
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                                                                                                                                                                           15-AUG-2002
                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 14; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-444169/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2002
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                                                                                                                                                                                                                                                                                                       disease;
                                          HALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVPIAQKSE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                          INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                     2000AU-0005995
Ekert PG,
                                                                                                                                                                                                                                                                                                       immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Betz
  Vaux DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human second mitochondria for identifying candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olejniczak
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                                                                                                                                                                                                                                                                                                                                                                                                                                        #15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                       disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide or DIABLO. DIABLO, or a nucleic acid encoding DIABLO, is useful for screening for an agent which modulates cell death. An antigen-binding molecule is useful for detecting DIABLO in a biological sample. The agent which modulates the level and/or functional activity of a polypeptide comprising mature or pro-human DIABLO polypeptide, is useful for the treatment and/or prophylaxis of a condition associated with expression or activation of DIABLO, such as cancer, vascular disease, hepatic disease, autoimmune disease and neurodegenerative disease, tissue damage or muscular tissue damage associated with heart attack, or hepatic tissue damage associated with a liver disease.
                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with an IAP and detecting the presence of an IAP/DIABLO complex), modulating the death of a cell (by contacting a cell with an agent, which modulates the level and/or functional activity of a polypeptide), a composition for treatment/prophylaxis of a DIABLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   active fragment of DIABLO (by contacting an inhibitor of apoptosis with a fragment of the polypeptide, and detecting a reduction in account of the IAP), producing a natural or synthetic variant of DIABLO with cell death activity or which reduces IAP activity, an antigenbinding molecule that specifically binds to DIABLO or its fragment, detecting DIABLO in a biological sample (by contacting the sample
               31-MAR-2000;
23-AUG-2000;
                                                                 30-MAR-2001; 2001WO-US08631
                                                                                                        11-OCT-2001
                                                                                                                                          WO200175067-A2
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                      Novel human diagnostic protein #24789
                                                                                                                                                                                                                                                                                                              18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                   ABG24798;
                                                                                                                                                                                                                                                                                                                                                                                      ABG24798 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIABLO is also useful for treatment and/or prophylaxis of conditions associated with cell death or apoptosis. The present sequence represents a partial peptide sequence from human DIABLO, identified by protein sequencing of a protein (later identified as DIABLO) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  death or apoptosis e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pro-apoptotic polypeptide, useful for screening for agents which modulate cell death and for treating conditions associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  co-precipitates with the human IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition comprising an agent which reduces the level/activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression vectors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated pro-apoptotic polypeptide, ignated DIABLO, or its biologically active fragment of 8 ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Page 4; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVSLVTDST 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
               2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LO, or its biologically active fragment of 8 amin
included are the polynucleotide encoding DIABLO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformed host cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pred. No. 21;

Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein MIHA (not defined).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   producing a biologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IAP)
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RESULT 11
ABB76218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                             DIABLO;
                                                                                 WO200230959-A2
                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human smac (DIABLO) derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB76218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB76218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food employed.
                                                                                                                                                                                                                                                                                                                                                                                                                 human; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS88985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPIAQKSEPHSLSSEALMRRAVS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPVHQQMRMHNVAGRATVRQQIS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; mutant; mutein
                                                                                                                                                                                                                                 Location/Qualifiers 5
                                                                                                                                          /note-
                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.7%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                               "wild-type Ala substituted by Phe"
                                                                                                                                          "optional C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB
Pred. No. 32;
9; Mismatches
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32;
                                                                                                                                      protecting group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 12
ABB76221
ID ABB76
XX
AC ABB76
XX
DT 09-AI
XX
DE Huma
XX
DE Huma
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DE Homc
OS Syni
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OS Syni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                second mitochondria derived activator of caspase (smac), also known cas direct inhibitor of apoptosis binding protein with low pi (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. CK (values for Bir-3 and Bir-2 are 0.5 +/- 0.1 uM and 2.5 +/- 0.0 c uM, respectively, for the present peptide, compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively, for full-length smac.

Amino acids C-terminal to the isoleucine of smac (DIABLO) are not important for binding to XIAP. The claimed peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide derived from wild-type activator of caspase protein useful f substances to kill cancerous cells -
                                                                                                                                                                                                                    Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a peptide derived from wild-type human second mitochondria derived activator of caspase (smac), also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
                13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                                                         DIABLO; smac;
                                                                                                                                                                                                                                                                                                    Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                  09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                              ABB76221;
                                                                                                                                                                                                                                                                                                                                                                                        ABB76221 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fesik SW,
                                         12-OCT-2001; 2001WO-US32121
                                                                       18-APR-2002
                                                                                                    WO200230959-A2
                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                            human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            smac (DIABLO) peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-2000; 2000US-0687549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001;
                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-444169/47.
                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 7; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVPFAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US32121
                                                                                                                                                                                                                                                          inhibitor of cytostatic;
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                             /note= "optional C-terminal protecting group
                                                                                                                                                         /note= "wild-type Ala substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Betz SP,
                                                                                                                                                                                                                                                          apoptosis protein; IAP; apoptosis;
mutant; mutein.
                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human second mitochondria derived for identifying candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뗩,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DIABLO), but has the native N-terminal alanine residue (see ABB76209) replaced by glycine. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for main and Bir-2 were each over 1,000 uM for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding N-terminal Ala peptide. The claimed smac-derived peptides can be used to identify confident apportunity of the corresponding N-terminal Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-2000;
                                                                                                                                                          Modified-site
                                                                                                                                                                                              Key
                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                         human;
                                                                                                                                                                                                                                                                      DIABLO;
                                                                                                                                                                                                                                                                                             Human smac
                                                                                                                                                                                                                                                                                                                     09-AUG-2002
                                                                                                                                                                                                                                                                                                                                             ABB76222;
                                                                                                                                                                                                                                                                                                                                                                    ABB76222 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  direct inhibitor of apoptosis binding protein with low pI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 15; 26pp; English
                     (ABBO ) ABBOTT LAB
                                                                     12-OCT-2001; 2001WO-US32121
                                                                                              18-APR-2002
                                                                                                                     WO200230959-A2
                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide and an IAP family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fesik SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conserv
                                                                                                                                                                                                                                                       smac; inhibitor of apoptosis protein;
cancer; cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meadows RP,
                                                                                                                                                                                                                                                                                             (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is a peptide derived from human se derived activator of caspase (smac), also
                                              2000US-0687549
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                             /note=
                                                                                                                                                                   /note= "wild-type Val substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%; 5.
100.0%; Pr
                                                                                                                                             "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Betz SP,
                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olejniczak ET,
                                                                                                                                                                                                                                                                   IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                      Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             known
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Fesik SW,

Meadows RP,

Betz SP,

Liu

2,

Olejniczak ET,

Sun

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RESULT 14
ABB76225
ID ABB76
XX
ABB7626
AC ABB76
XX
DT 09-AI
XX
DIAB
KW DIAB
XX
DOS HOME
OS Syni
XX
FT Mis
FT Moc
FT Moc
FT MOC
XX
PN WO:
XX
PP 12
XX
PR 11:
XX
PR 11:
XX
PR 12
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PR 11:
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XX
XX
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DIABLO), but has the native valine residue (see ABB76209) replaced by alanine. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis protein (IAP) family member. Mutation of the valine of the peptide causes some loss of binding to the protein. Thus, Kd values for Bir-3 and Bir-2 were 12 +/- 2 uM and 56 +/- 5 uM, respectively, uM for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding wild-type peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to
                 WPI; 2002-444169/47
                                             Fesik SW,
                                                                       (ABBO ) ABBOTT LAB
                                                                                                   13-OCT-2000; 2000US-0687549
                                                                                                                              12-OCT-2001; 2001WO-US32121
                                                                                                                                                           18-APR-2002
                                                                                                                                                                                       W0200230959-A2
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          DIABLO;
                                                                                                                                                                                                                                                                                                                                                                                    Human smac (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB76225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76225 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a peptide derived from human second mitochondria derived activator of caspase (smac), also known as direct inhibitor of apoptosis binding protein with low pI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disrupt the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-444169/47.
                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                             smac;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVPIAQKSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAPIAQKSE
                                            Meadows RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                      inhibitor of apoptosis protein; IAP; apoptosis;
                                                                                                                                                                                                                                                                                                                                           cytostatic; mutant; mutein.
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interaction between a smac peptide and an IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26pp; English.
                                                                                                                                                                                                             "optional C-terminal protecting group
                                                                                                                                                                                                                                         "wild-type Ala substituted by Gly"
                                          Betz SP,
                                                                                                                                                                                                                                                                                                                                                                                   peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                          Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                          Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3e+05;
                                       Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                          ET,
                                          Sun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 15
ABB76226
    CC The present sequence is a peptide derived from human second CC mitochondria derived activator of caspase (smac), also known as CC direct inhibitor of apoptosis binding protein with low pI CC (DIABLO), but has the native Ala residue (see ABB76209) replaced CC by glycine. Claimed smac-derived pertides (see ABB76208-19) bind CC to the Bir2 and Bir3 domain of XIAP, an inhibitor of apoptosis CC protein (IAP) family member. Mutation of the amino acids CC claimed stream of binding to the protein. Thus, Kd values for CC claimed little loss of binding to the protein. Thus, Kd values for CC claimed bir-2 were 1.2 +/- 0.4 uM and 10 +/- 2 uM, respectively, CC uM for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 the claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay C involves determination of the ability of candidate of amily member.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate
                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                              DIABLO; smac;
                                          WPI; 2002-444169/47.
                                                                   Fesik SW, Meadows RP,
                                                                                            (ABBO ) ABBOTT LAB
                                                                                                                      13-OCT-2000; 2000US-0687549
                                                                                                                                               12-OCT-2001; 2001WO-US32121
                                                                                                                                                                            18-APR-2002
                                                                                                                                                                                                     WO200230959-A2
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                     human;
                                                                                                                                                                                                                                                                                                                                                                                          Human smac
                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB76226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB76226 standard;
                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide derived from wild-type human second mitochondria derived activator of caspase protein useful for identifying candidate substances to kill cancerous cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVPIAQKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVPIGQKSE
                                                                                                                                                                                                                                                                                                                                                                                         (DIABLO) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                  inhibitor of apoptosis protein; IAP; apoptosis;
cytostatic; mutant; mutein.
                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                        /note= "n-propionic acid"
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
88
                                                                                                                                                                                                                             "optional C-terminal protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9%;
                                                                   Betz
                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38;
Pred. No.
                                                                   SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                   Liu
                                                                  z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )В __
).3e+05;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                Olejniczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                  ET,
                                                                  Sun
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Вb
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Search completed: October 2, 2003, 09:41:55
Job time : 36 secs
                                                                                                                                                                                                                                                                                                                    The present sequence is a peptide derived from human second control mitochondria derived activator of caspase (smac), also known as condition of depotes in with low pI (DIABLO), but has the native N-terminal alanine residue (see ABB76209) replaced by propionic acid. Claimed smac-derived peptides (see ABB76209) replaced by propionic acid. Claimed smac-derived peptides (see ABB76209) replaced by propionic acid. Claimed smac-derived peptides (see ABB76208-19) bind to the Bir2 and Bir3 domain of XIAP, an ocid inhibitor of apoptosis protein (IAP) family member. Modification of the N-terminal alanine destroys all binding affinity for the protein. Thus, Kd values for Bir-3 and Bir-2 were each over 1,000 cum for the present peptide, compared with 0.43 +/- 0.06 uM and 6.0 +/- 0.9 uM, respectively, for the corresponding N-terminal Ala peptide. The claimed smac-derived peptides can be used to identify candidate substances which induce or promote apoptosis in cells. The assay involves determination of the ability of candidate compounds to disrupt the binding interaction between a smac compensation of the ability of candidate peptide and an IAP family member.
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 15; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substances to kill cancerous cells
                                                                                         2 VPIAQKSE 9
|||||||
2 VPIAQKSE 9
                                                                                                                                                                                                                                                                                  9 AA;
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                            27.0%; Score 38; 100.0%; Pred. No.
                                                                                                                                                                                    0;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                       DB 23; Length 9;
9.3e+05;
                                                                                                                                                                                    0; Indels
                                                                                                                                                                                    0;
                                                                                                                                                                                  Gaps
                                                                                                                                                                                    0;
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